



01-21-00

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Attorney Docket No.: 5808.200-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

FILING UNDER 37 C.F.R. 1.53(b)



Box Patent Application
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Express Mail Label No. EL293692871US
Date of Deposit January 20, 2000

Sir:

This is a request for filing a patent application under 37 C.F.R. 1.53(b) of

Applicant(s): Martin Lehmann

Title: Improved Phytases

75 pages of specification 56 sheets of drawings

3 sheets of Declaration and Power of Attorney

The filing fee is calculated as follows:

Basic Fee: \$ 690.00

Total Claims: $14 - 20 = 0 \times 18 =$ \$0

Independent Claims: $9 - 3 = 6 \times 78 =$ \$ 468.00

Total Fee: \$1,158.00

Priority of Danish application nos. PA 1999 00092 and PA 1999 01340 filed on January 22, 1999 and September 21, 1999 is claimed under 35 U.S.C. 119. A certified copy is submitted herewith.

Priority of U.S. provisional application nos. 60/117,659 and 60/156,495 filed on January 28, 1999 and September 28, 1999 is claimed under 35 U.S.C. 119.

Please amend the specification as follows: At page 1, after the title, insert Cross-Reference to Related Applications

This application claims priority of provisional application nos. 60/117,659 and 60/156,495 filed on January 28, 1999 and September 28, 1999 and of Danish application

nos. PA 1999 00092 and PA 1999 01340 filed January 22, 1999 and September 21, 1999, the contents of which are fully incorporated herein by reference.

Address all future communications to Steve T. Zelson, Esq., Novo Nordisk of North America, Inc., 405 Lexington Avenue, Suite 6400, New York, NY 10174-6401.

Please charge the required fee, estimated to be \$1,158, to Novo Nordisk of North America, Inc., Deposit Account No. 14-1447. A duplicate of this sheet is enclosed.

Respectfully submitted,

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

EXPRESS MAIL CERTIFICATE

Box Patent Application
Assistant Commissioner for Patents
Washington, DC 20231

Re: U.S. Patent Application for
Title: Improved Phytases
Applicants: Martin Lehmann

Sir:

Express Mail Label No. EL293692871US

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Improved phytases

Phytases are enzymes that hydrolyze phytate (myo-inositol hexakisphosphate) to myo-inositol and inorganic phosphate. They
5 are known to be valuable feed additives.

The present invention relates to improved phytases, viz. phytases of amended characteristics, e.g. amended activity characteristics, reference being made to e.g. the phytase(s) it has been derived from, or to known phytases. Amended activity
10 characteristics means amended in at least one phytase activity related respect, such as (non-exclusive list): pH stability, temperature stability, pH profile, temperature profile, specific activity (in particular in relation to pH and temperature), substrate specificity, substrate cleavage pattern, substrate
15 binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate), end level of released phosphate reached.

Examples of amended activity characteristics are amended specific activity (e.g. increased, e.g. increased at a pH of 3,
20 4, 5, or 6); amended pH or temperature profile; and/or amended (e.g. increased) thermostability, e.g. of an increased melting temperature as measured using Differential Scanning Calorimetry (DSC).

The present invention also relates to a process for the
25 preparation of a modified protein, wherein in a first step a consensus sequence is determined from a number of highly homologous sequences according to steps a), b) and c) below:

a) at least three, preferably at least four amino acid sequences are aligned by any standard alignment program known in
30 the art;

b) at every position of the amino acid sequence alignment, the amino acids are evaluated for their evolutionary similarity and a consensus residue is chosen by any standard program known in the art, whereby the minimal requirements for calculation of 5 a consensus residue are set in such a way that the program is already able to determine a consensus residue if a given residue occurs in only two of the aligned sequences. However, if there is a subgroup of sequences among the compared amino acid sequences that shows a much higher degree of similarity with 10 each other than with the remaining sequences of the alignment, the subgroup may be represented in the calculation only with its consensus sequence determined in the same way as outlined in EP 897985, or alternatively, to each sequence of the subgroup, a vote weight of 1 divided by the number of sequences in the 15 subgroup will be assigned;

c) in case no consensus amino acid at a defined position is identified by the program, any of the amino acids, preferably the most frequently occurring amino acid at this position is selected.

20 In a second aspect of the invention, a homologous sequence is compared with the consensus sequence, and one or more non-consensus residues in this homologous sequence are replaced by the corresponding consensus residues.

Preferably, only such amino acid residues are replaced in 25 the homologous amino acid sequence where a consensus residue can clearly be defined by the program under moderately stringent conditions whereas at all positions of the alignment where no preferred consensus amino acid can be determined under moderately stringent conditions, the amino acids of the 30 homologous protein remain unchanged.

In a third aspect of the invention, the active center of the protein of interest is determined, comprising all amino acid residues that are involved in forming the active center, both in the consensus sequence, and in the sequence of a homologous protein; subsequently, some or all of the divergent amino acid residues of the homologous protein are inserted in the backbone of the consensus sequence.

In one embodiment of this process, the program used for the comparison of amino acids at a defined position regarding their evolutionary similarity is the program "PRETTY".

The active center of the protein can be determined by using an analysis of the three-dimensional structure of the protein.

An example of a homologous protein is an enzyme family, an example of a defined protein family is the family of phytases, e.g. of fungal origin.

For example, the amino acid sequence of the phytase can be changed by the introduction of at least one mutation or substitution chosen from

| | | |
|----|-------|-------|
| 20 | E58A | F54Y |
| | D69K | I73V |
| | D197N | K94A |
| | T214L | R101A |
| | E222T | N153K |
| 25 | E267D | V158I |
| | R291I | A203G |
| | R329H | S205G |
| | S364T | V217A |
| | A379K | A227V |
| 30 | G404A | V234L |
| | | P238A |

Q277E

A287H

A292Q

V366I

5 A396S

E415Q

G437A

R451E

For interpreting these abbreviations, as an example, the
 10 mutation E58A is to be interpreted as follows: When subtracting
 26 from the number, you get the position or residue number in
 the consensus phytase sequence or another phytase sequence
 aligned as shown in Fig. 1 (corresponding to the addition of a
 26 amino acid signal sequence to the sequences shown in Fig. 1).
 15 For example, in E58A, number 58 means position number 32 (58-
 26=32). And the letter before the number, i.e. E, represents the
 amino acid in the phytase to be modified which is replaced by
 the amino acid behind the number, i.e. A.

The above-mentioned amino acid replacements, alone and/or
 20 in combination, have a positive effect on the protein stability.

The following sub-groups of mutations are also interesting
 (i.e. phytases comprising at least one mutation selected from
 either one of the groups of):

E58A, D69K, D197N, T214L, E222T, E267D, R291I, R329H,

25 S364T, A379K, G404A;

F54Y, I73V, K94A, R101A, N153K, V158I, A203G, S205G,
 V217A, A227V, V234L, P238A, Q277E, A287H, A292Q, V366I, A396S,
 E415Q, G437A, R451E;

E58A, D69K, D197N, F54Y, I73V, K94A;

30 T214L, E222T, E267DR101A, N153K, V158I;

R291I, R329H, S364TA203G, S205G, V217A;

A379K, G404AA227V, V234L, P238A, Q277E;
A287H, A292Q, V366I, A396S, E415Q, G437A, R451E;
T214L, E222T, S364T, V158I, A203G, G404A, A227V, P238A,
A396S, G437A, R451E.

5 Examples of host cells are plant cells, animal cells, and microbial cells, e.g. prokaryotic or eukaryotic cells, such as bacterial, fungal or yeast cells. An example of a fungal host is a strain of the genus *Aspergillus*, and examples of yeast hosts are strains of *Saccharomyces*, and strains of *Hansenula*.

10 The invention also relates to a modified protein obtainable or obtained by any of the processes described above.

The invention also relates to a variant or mutein of a phytase such as (but not limited to) the consensus phytase-1, wherein, in the amino acid sequence in Figure 2, at least one 15 of the following replacements have been effected: Q50L, Q50T, Q50G, Q50T-Y51N, Q50L-Y51N or Q50T-K91A.

In the third aspect mentioned above, a consensus sequence is determined from homologous sequences as described above; in a second step the active center of the protein comprising all 20 amino acid residues that are involved in forming the active center is determined in the consensus sequence and in the sequence of a single homologous protein as well. The single homologous protein may have preferred properties like high specific activity or different pH dependency of enzymatic 25 activity. In a third step some or all amino acid residues that are involved in forming the active center of the homologous protein are inserted into the backbone of the consensus sequence. The result thereof is a chimeric protein having the active center derived from a single protein and the backbone of 30 the consensus sequence.

The active center of the protein can be determined e.g. by using any analysis of the three-dimensional structure of the protein, e.g. by homology modelling on the basis of a known 3D-structure of a known protein.

5 The present invention also provides consensus proteins obtainable or obtained by such processes, in particular proteins comprising at least one of the amino acid sequences shown in Figures 2-6, 10 or 21, or variants or muteins thereof. Examples of such variants are shown in Figs. 7-9.

10 Such variants or muteins can be defined and prepared on the basis of the teachings given in European Patent Application number 0897010, e.g. Q50L, Q50T, Q50G, Q50L-Y51N, or Q50T-Y51N. These mutations are defined as above, or, alternatively, by reference to Fig. 2. When referring to Fig. 2, no subtraction of
15 the 26 amino acid signal peptide is required (e.g. in "Q50L," at position 50 of the amino acid sequence of Fig. 2, the amino acid Q has been replaced by amino acid L).

A food, feed, or pharmaceutical composition comprising the phytases of the invention is another aspect of the invention.

20 In this context, and relating to the process of the invention, "at least three, preferably at least four amino acid sequences of such defined protein family" means that three, four, five, six to twelve, twenty, fifty, or even more sequences can be used for the alignment and the comparison to create the
25 amino acid sequence of the consensus protein. "Sequences of a defined protein family" means that such sequences fold into a three-dimensional structure, wherein the alpha-helices, the beta-sheets and beta-turns are at the same position so that such structures are, as called by the man skilled in the art, largely
30 superimposable. Furthermore these sequences characterize proteins that show the same type of biological activity, e.g. a

defined enzyme class, e.g. the phytases. The three-dimensional structure of one such protein is sufficient to allow the modelling of the structure of the other homologous proteins of such a family. An example, how this can be done, is given in

5 Example 1. "Evolutionary similarity" in the context of the present invention refers to a scheme which classifies amino acids regarding their structural similarity which allows that one amino acid can be replaced by another amino acid with a minimal influence on the overall structure, as this is done e.g.

10 by programs, like "PRETTY", known in the art. The phrase "the degree of similarity provided by such a program...is set to less stringent number" means in the context of the present invention that values for the parameters which determine the degree of similarity in the program used in the practice of the present

15 invention are chosen in a way to allow the program to define a consensus amino acid for a maximum of positions of the whole amino acid sequence, e. g. in case of the program PRETTY a value of 2 or 3 for the THRESHOLD and a value of 2 for the PLURALITY can be chosen. Furthermore, "a vote weight of one divided by the

20 number of such sequences" means in the context of the present invention that the sequences which define a group of sequences with a higher degree of similarity as the other sequences used for the determination of the consensus sequence only contribute to such determination with a factor which is equal to one

25 divided by the number of all sequences of this group.

As mentioned before, should the program not allow to select the consensus amino acid, the most frequent amino acid is selected; should the latter be impossible the man skilled in the art will select an amino acid from all the sequences used for 30 the comparison which is known in the art for its property to improve the thermostability in proteins as discussed e.g. by

Janecek, S. (1993), Process Biochem. 28, 435-445; Fersht, A. R. & Serrano, L. (1993), Curr. Opin. Struct. Biol. 3, 75-83; Alber, T. (1989), Annu. Rev. Biochem. 58, 765-798; Matthews, B. W. (1987), Biochemistry 26, 6885-6888; or Matthews, B. W. (1991),
5 Curr. Opin. Struct. Biol. 1, 17-21.

The stability of an enzyme is relevant for many industrial applications. Therefore, a lot of attempts, more or less successful, have been made to improve the stability, preferably the thermostability of enzymes by rational or random approaches.

10 Here we present an alternative way to improve the thermostability of a protein.

The invention provides a process for the preparation of a consensus protein comprising a process to calculate an amino acid residue for nearly all positions of a so-called consensus
15 protein and to synthesize a complete gene from this sequence that can be expressed in a pro- or eukaryotic expression system.

DNA sequences of the present invention can be constructed starting from genomic or cDNA sequences encoding the proteins, e.g. phytases, of interest. For example, they can be constructed
20 by methods of in vitro mutagenesis [see e.g. Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratory Press, New York]. A widely used strategy for "site-directed mutagenesis", as originally outlined by Hurchinson and Edgell [J. Virol. 8, 181 (1971)], involves the annealing of a synthetic
25 oligonucleotide carrying the desired nucleotide substitution to a target region of a single-stranded DNA sequence wherein the mutation should be introduced [for review see Smith, Annu. Rev. Genet. 19, 423 (1985), and for improved methods, see references 2-6 in Stanssen et al., Nucl. Acids Res., 17, 4441-4454 (1989)].
30 Another possibility of mutating a given DNA sequence is the mutagenesis by using the polymerase chain reaction (PCR). DNA as

starting material can be isolated by methods known in the art and described e.g. in Sambrook et al. (Molecular Cloning) from the respective strains.

For strain information, see e.g. EP 684313 or any 5 depository authority indicated below. *Aspergillus niger* [ATCC 9142], *Myceliophthora thermophila* [ATCC 48102], *Talaromyces thermophilus* [ATCC 20186] and *Aspergillus fumigatus* [ATCC 34625] have been redeposited according to the conditions of the Budapest Treaty at the American Type Culture Cell Collection 10 under the following accession numbers: ATCC 74337, ATCC 74340, ATCC 74338 and ATCC 74339, respectively. It is, however, understood that DNA encoding a consensus protein in accordance with the present invention can also be prepared in a synthetic manner as described, e.g. in EP 747483 or EP 897985, or in the 15 examples, by methods known in the art.

For sequence information, see e.g. EP 684313, or sequence data bases, for example like Genbank (Intelligenetics, California, USA), European Bioinformatics Institute (Hinstone Hall, Cambridge, GB), NBRF (Georgetown University, Medical 20 Centre, Washington DC, USA) and Vecbase (University of Wisconsin, Biotechnology Centre, Madison, Wisconsin, USA).

The process of the present invention can e.g. be used to improve the thermostability of the enzyme phytase.

Once complete DNA sequences of the present invention have 25 been obtained they can be integrated into vectors by methods known in the art and described e.g. in Sambrook et al. (s.a.) to overexpress the encoded polypeptide in appropriate host systems. However, a man skilled in the art knows that also the DNA sequences themselves can be used to transform the suitable host 30 systems of the invention to get overexpression of the encoded polypeptide. Appropriate host systems are for example fungi,

like Aspergilli, e.g. *Aspergillus niger* [ATCC 9142] or *Aspergillus ficuum* [NRRL 3135] or like *Trichoderma*, e.g. *Trichoderma reesei*; or yeasts, like *Saccharomyces*, e.g. *Saccharomyces cerevisiae* or *Pichia*, like *Pichia pastoris*, or 5 *Hansenula polymorpha*, e.g. *H. polymorpha* (DSM5215); or plants, as described, e.g. by Pen et al., Bio/Technology 11, 811-814 (1994). A man skilled in the art knows that such microorganisms are available from depository authorities, e.g. the American Type Culture Collection (ATCC), the Centraalbureau voor 10 Schimmelcultures (CBS) or the Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH (DSM) or any other depository authority as listed in the Journal "Industrial Property" [(1991) 1, pages 29-40]. Bacteria which can be used are e.g. *E. coli*; *Bacilli* as, e.g., *Bacillus subtilis*; or 15 *Streptomyces*, e.g. *Streptomyces lividans* (see e.g. Anné and Mallaert in FEMS Microbiol. Lett. 114, 121 (1993)). Preferred *E. coli* strains, which can be used are *E. coli* K12 strains e.g. M15 [described as DZ 291 by Villarejo et al. in J. Bacteriol. 120, 466-474 (1974)], HB 101 [ATCC No. 33694] or *E. coli* SG13009 20 [Gottesman et al., J. Bacteriol. 148, 265-273 (1981)].

Vectors which can be used for expression in fungi are known in the art and described e.g. in EP 420358, or by Cullen et al. [Bio/Technology 5, 369-376 (1987)], Ward [Molecular Industrial Mycology, Systems and Applications for Filamentous 25 Fungi, Marcel Dekker, New York (1991)], Upshall et al. [Bio/Technology 5, 1301-1304 (1987)], Gwynne et al. [Bio/Technology 5, 71-79 (1987)], or Punt et al. [J. Biotechnol. 17, 19-34 (1991)]; and for yeasts by Sreekrishna et al. [J. Basic Microbiol. 28, 265-278 (1988), Biochemistry 28, 4117-4125 30 (1989)], Hitzemann et al. [Nature 293, 717-722 (1981)] or in EP 183070, EP 183071, EP 248227, or EP 263311. Suitable vectors

which can be used for expression in *E. coli* are mentioned, e.g. by Sambrook et al. [s.a.], Fiers et al. [Procd. 8th Int. Biotechnology Symposium", Soc. Franc. de Microbiol., Paris (Durand et al., eds.), pp. 680-697 (1988)], Bujard et al. [Meth. Enzymol. 155, 416-433 (1987)], or Stüber et al. [Immunological Methods, eds. Lefkovits and Pernis, Academic Press, Inc., Vol. IV, 121-152 (1990)]. Vectors that can be used for expression in *Bacilli* are known in the art and described, e.g. in EP 207459, EP 405370, Proc. Natl. Acad. Sci. USA 81, 439 (1984) or Yansura and Henner, Meth. Enzymol. 185, 199-228 (1990). Vectors which can be used for the expression in *H. Polymorpha* are known in the art and described, e.g. in Gellissen et al., Biotechnology 9, 291-295 (1991).

Either such vectors already carry regulatory elements, e.g. promotors, or the DNA sequences of the present invention can be engineered to contain such elements. Suitable promotor elements which can be used are known in the art and are, e.g. for *Trichoderma reesei* the cbh1- [Haarki et al., Biotechnology 7, 596-600 (1989)] or the pkil-promotor [Schindler et al., Gene 130, 271-275 (1993)]; for *Aspergillus oryzae* the amy-promotor [Christensen et al., Abstr. 19th Lunteren Lectures on Molecular Genetics F23 (1987), Christensen et al., Biotechnology 6, 1419-1422 (1988), Tada et al., Mol. Gen. Genet. 229, 301 (1991)]; and for *Aspergillus niger* the glaA- [Cullen et al., Bio/Technology 5, 369-376 (1987), Gwynne et al., Bio/Technology 5, 713-719 (1987), Ward in Molecular Industrial Mycology, Systems and Applications for Filamentous Fungi, Marcel Dekker, New York, 83-106 (1991)], alcA- [Gwynne et al., Bio/Technology 5, 718-719 (1987)], suc1- [Boddy et al., Curr. Genet. 24, 60-66 (1993)], aphA- [MacRae et al., Gene 71, 339-348 (1988), MacRae et al., Gene 132, 193-198 (1993)], tpiA- [McKnight et al., Cell 46, 143-

147 (1986), Upshall et al., Bio/Technology 5, 1301-1304 (1987)],
gpdA- [Punt et al., Gene 69, 49-57 (1988), Punt et al., J.
Biotechnol. 17, 19-37 (1991)] and the pkiA-promotor [de Graaff
et al., Curr. Genet. 22, 21-27 (1992)]. Suitable promotor
elements that can be used for expression in yeast are known in
the art and are, e.g. the pho5-promotor [Vogel et al., Mol.
Cell. Biol., 2050-2057 (1989); Rudolf and Hinnen, Proc. Natl.
Acad. Sci. 84, 1340-1344 (1987)] or the gap-promotor for
expression in *Saccharomyces cerevisiae*; the aox1-promotor [Koutz
et al., Yeast 5, 167-177 (1989); Sreekrishna et al., J. Basic
Microbiol. 28, 265-278 (1988)] for *Pichia pastoris*; or the FMD
promoter [Hollenberg et al., EPA No. 0299108] or MOX-promotor
[Ledeboer et al., Nucl. Acids Res. 13, 3063-3082 (1985)] for *H.*
polymorpha.

15 Accordingly vectors comprising DNA sequences of the
present invention, preferably for the expression of said DNA
sequences in bacteria or a fungal or a yeast host and such
transformed bacteria or fungal or yeast hosts are also a part of
the invention.

20 The invention also provides a system that allows for high
expression of proteins, in particular of the phytases of the
invention, such as recombinant *Hansenula* strains. To achieve
that, the codons of the DNA sequence of such a protein may be
selected on the basis of a codon frequency table of the organism
25 used for expression, e.g. of yeast as in the present case (see
e.g. in Example 1). Optionally, the codons for the signal
sequence may be selected in a manner as described for the
specific case in Example 1; that means that a codon frequency
table is prepared on the basis of the codons used in the DNA
30 sequences which encode the amino acid sequences of the given
protein family. Then the codons for the design of the DNA

sequence of the signal sequence are selected from a codon frequency table of the host cell used for expression whereby always codons of comparable frequency in both tables are used.

Once such DNA sequences have been expressed in an appropriate host cell in a suitable medium, the encoded protein can be isolated either from the medium in the case the protein is secreted into the medium or from the host organism in case such protein is present intracellularly by methods known in the art of protein purification or described in case of a phytase, e.g. in EP 420358. Accordingly, a process for the preparation of a polypeptide of the present invention wherein transformed bacteria or a host cell as described above are cultured under suitable culture conditions, and the polypeptide is recovered therefrom and a polypeptide when produced by such a process; or a polypeptide encoded by a DNA sequence of the present invention, are also a part of the present invention.

Once obtained, the polypeptides of the present invention can be characterized regarding their properties that make them useful in agriculture by any assay known in the art.

In general, the polypeptides of the present invention can be used without being limited to a specific field of application, e.g. in case of phytases for the conversion of inositol polyphosphates, like phytate, to inositol and inorganic phosphate.

Furthermore, the polypeptides of the present invention can be used in a process for the preparation of a pharmaceutical composition or compound food or feeds wherein the components of such a composition are mixed with at least one polypeptide of the present invention. Accordingly, compound food or feeds or pharmaceutical compositions comprising at least one polypeptide of the present invention are also a part of the present

invention. A man skilled in the art is familiar with their process of preparation. Such pharmaceutical compositions or compound foods or feeds can further comprise additives or components generally used for such purpose and known in the 5 state of the art.

The present invention also provides a process for the reduction of levels of phytate in animal manure wherein an animal is fed such a feed composition in an amount effective in converting phytate contained in the feedstuff to lower inositol 10 phosphates and/or inositol, and inorganic phosphate.

In the present context, a phytase is an enzyme or polypeptide that has phytase activity. A phytase can be e.g. a myo-inositol hexakisphosphate phosphohydrolase, such as (myo-inositol hexakisphosphate 3-phosphohydrolase, EC 3.1.3.8) and 15 (myo-inositol hexakisphosphate 6-phosphohydrolase, EC 3.1.3.26).

In one embodiment, the phytase is purified, viz. at least 85%, preferably at least 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% pure, as evaluated by SDS-PAGE. The phytase may be isolated. Phytase activity can be determined using any 20 phytase assay known in the art, e.g. the assay described herein (see Example 9). The assay temperature may be the optimum temperature of the actual phytase, and the assay pH may be the optimum pH of the actual phytase.

The assay temperature may e.g. be selected within the 25 range of 20-90°C, or 30-80°C, or 35-75°C, for instance temperatures of 37°C, 50°C, 60°C, or 70°C.

The assay pH may e.g. be selected within the range of pH 2-9, or 3-8, or 3-6, for instance assay pH values of 3, 4, 5, 6, or 7 may be chosen.

30 Amino acid sequence homology (or polypeptide or amino acid homology) is determined as the degree of identity between two

sequences. This may suitably be determined by means of computer programs known in the art such as GAP provided in the GCG program package [Program Manual for the Wisconsin Package, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin 5 53711, USA], see also Needleman, S.B. and Wunsch, C.D., (1970), J. Mol. Biol., 48, 443-453]. In release 9.1, for comparing polypeptide sequences, the Length Weight is set to 0, and the Gap Weight is set to 3.0.

The degree of identity or homology between two DNA 10 (nucleic acid) sequences may be determined by means of computer programs known in the art such as GAP provided in the GCG program package [Program Manual for the Wisconsin Package, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin 53711, USA], see also Needleman, S.B. and Wunsch, C.D., (1970), 15 J. Mol. Biol., 48, 443-453]. In release 9.1, GAP is used with the following settings for DNA sequence comparison: GAP creation penalty of 50 and GAP extension penalty of 3.

Suitable experimental conditions for determining whether a given DNA or RNA sequence hybridizes to a specified nucleotide 20 or oligonucleotide probe involves presoaking of the filter containing the DNA or RNA fragments to examine for hybridization in 5 x SSC (Sodium chloride/Sodium citrate; (J. Sambrook, E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning, A Laboratory Manual, 2nd edition, Cold Spring Harbor, New York) for 10 min, 25 and prehybridization of the filter in a solution of 5 x SSC, 5 x Denhardt's solution, 0.5 % SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook et al. 1989), followed by hybridization in the same solution containing a concentration of 10 ng/ml of a random-primed (Feinberg, A. P. and Vogelstein, B. 30 (1983) Anal. Biochem. 132:6-13), ^{32}P -dCTP-labeled (specific

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activity > 1 x 10⁹ cpm/μg) probe for 12 hours at approximately 45°C.

The filter is then washed twice for 30 minutes in 2 x SSC, 0.5 % SDS at at least 55°C (low stringency), at at least 60°C 5 (medium stringency), at at least 65°C (medium/high stringency), at at least 70°C (high stringency), or at at least 75°C (very high stringency).

Molecules to which the oligonucleotide probe hybridizes under these conditions can be detected using an x-ray film.

10 Phytases of amended thermostability, or thermostable phytases, are one aspect of the present invention. A "thermostable" phytase is a phytase that has a T_m (melting temperature) - as measured on purified phytase protein by Differential Scanning Calorimetry (DSC) - of at least 65°C. For 15 the DSC, a constant heating rate may be used, e.g. of 10°C/min. In alternative embodiments, the T_m is at least 66, 67, 68, 69, 70, 71, 72, 73, 74 or 75°C. Or, the T_m is equal to or lower than 150°C, or equal to or lower than 145, 140, 135, 130, 125, 120, 115 or 110°C. Accordingly, examples of intervals of T_m are: 65- 20 150°C, 66-150°C, - (etc.) - 75-150°C; 65-145°C, 66-145°C, - (etc.) - 75-145°C; 65-140°C, - (etc.) - 75-140°C; - (etc.) - 65- 110°C, 66-110°C, - (etc.) - 75-110°C.

Particular ranges for T_m are the following: between 65 and 110°C; between 70 and 110°C; between 70 and 100°C; between 75 25 and 95°C, or between 80 and 90°C.

In Examples 9 and 10 below, the measurement of T_m by DSC is described, and the T_m's of a number of phytases are shown.

The optimum temperatures are also indicated, since - as an alternative mean - a thermostable phytase can be defined as a 30 phytase having a temperature-optimum of at least 60°C. Preferably, the optimum temperature is determined on the

substrate phytate or phytic acid at pH 5.0 or 5.5. Example 9 describes an example of a phytase assay, including a definition of units.

In alternative embodiments, the optimum temperature is at least 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70°C. In a particular embodiment, the optimum temperature is equal to or lower than 140°C, or equal to or lower than 135, 130, 125, 120, 115, 110, 105 or 100°C. Accordingly, examples of intervals of optimum temperature are: 60-140°C, 61-140°C, - (etc.) - 70-140°C; 60-135°C, 61-135°C, - (etc.) - 70-135°C; 60-130°C, - (etc.) - 70-130°C; - (etc.) - 60-100°C, 61-100°C, - (etc.) - 70-100°C.

Before describing the present invention in more detail a short explanation of the Figures enclosed is given below.

15

Figure 1: Design of the consensus phytase-1 sequence. The letters represent the amino acid residues in the one-letter code. The following sequences were used for the alignment: phyA from *Aspergillus terreus* 9A-1 [Mitchell, D. B., Vogel, K., Weimann, B. J., Pasamontes, L. & van Loon, A. P. G. M. (1997) The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fungi *Aspergillus terreus* and *Myceliophthora thermophila*, *Microbiology* 143, 245-252]; from amino acid (aa) 27; SEQ ID NO: 1]; phyA from *A. terreus* cbs116.46 [EP 897985]. A heat resistant phytase of *Aspergillus fumigatus* with superior performance in animal experiments. Phytase optimization and natural variability. In: *The Biochemistry of phytate and phytases* (eds. Rasmussen, S.K; Raboy, V.; Dalbøge, H. and Loewus, F.; Kluwer Academic Publishers); from aa 27; SEQ ID NO: 2; phyA from *Aspergillus niger* var. *awamori* (Piddington et al (1993) *Gene* 133, 55-62;

from aa 27; SEQ ID NO: 3); phyA from *A. niger* T213 (EP 897985); from aa 27; SEQ ID NO: 4); phyA from *A. niger* strain NRRL3135 [van Hartingsveldt, W., van Zeijl, C. M. F., Harteveld, G. M., Gouka, R. J., Suykerbuyk, M. E. G., Luiten, R. G. M., van 5 Paridon, P. A., Selten, G. C. M., Veenstra, A. E., van Gorcom, R. F. M., & van den Hondel, C. A. M. J. J. (1993) Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of *Aspergillus niger*. Gene 127, 87-94; from aa 27; SEQ ID NO: 5]; phyA from *Aspergillus fumigatus* ATCC 13073 (Pasamontes, 10 L., Haiker, M., Wyss, M., Tessier, M. & van Loon, A. P. G. M. (1997) Cloning, purification and characterization of a heat stable phytase from the fungus *Aspergillus fumigatus*, Appl. Environ. Microbiol. 63, 1696-1700; from aa 25; SEQ ID NO: 6]; phyA from *A. fumigatus* ATCC 32722 (EP 897985); from aa 27; SEQ 15 ID NO: 7); phyA from *A. fumigatus* ATCC 58128 (EP 897985); from aa 27; SEQ ID NO: 8); phyA from *A. fumigatus* ATCC 26906 (EP 897985); from aa 27; SEQ ID NO: 9); phyA from *A. fumigatus* ATCC 32239 (EP 897985); from aa 30; SEQ ID NO: 10; phyA from *Emericella nidulans* [Pasamontes, L., Haiker, M., Henriquez- 20 Huecas, M., Mitchell, D. B. & van Loon, A. P. G. M. (1997a). Cloning of the phytases from *Emericella nidulans* and the thermophilic fungus *Talaromyces thermophilus*. Biochim. Biophys. Acta 1353, 217-223; from aa 25; SEQ ID NO: 11]; phyA from *Talaromyces thermophilus* (Pasamontes et al., 1997a; from aa 24; 25 SEQ ID NO: 12); and phyA from *Myceliophthora thermophila* (Mitchell et al., 1997; from aa 19; SEQ ID NO: 13). The alignment was calculated using the program PILEUP. The location of the gaps was refined by hand. Capitalized amino acid residues in the alignment at a given position belong to the amino acid 30 coalition that establish the consensus residue. In bold, beneath the calculated consensus sequence, the amino acid sequence of

the finally constructed consensus phytase (Fcp) is shown (SEQ ID NO: 14). The gaps in the calculated consensus sequence were filled by hand according to principals stated in Example 1.

5 Figure 2: DNA sequence (SEQ ID NO: 15) of the consensus phytase-1 gene (fcp) and of the primers used for the gene construction. The calculated amino acid sequence (Figure 1, SEQ ID NO: 14) was converted into a DNA sequence using the program BACKTRANSLATE [Devereux, J., Haeberli, P. & Smithies, O. (1984)
10 A comprehensive set of sequence analysis programs for the VAX. Nucl. Acids Res. 12, 387-395], and the codon frequency table of highly expressed yeast genes (GCG program package, 9.0). The signal peptide of the phytase from *A. terreus* cbs 116.46 was fused to the N-terminus. The amino acid sequence shown in Fig. 2
15 is SEQ ID NO: 16. The bold bases represent the sequences of the oligonucleotides used to generate the gene. The names of the respective oligonucleotides are alternately noted above or below the sequence. The underlined bases represent the start and stop codon of the gene. The bases written in italics represent the
20 two introduced Eco RI sites.

25 Figure 3: Alignment and consensus sequence of five Basidiomycete phytases. The letters represent the amino acid residues in the one-letter code. The amino acid sequences of the phytases from *Paxillus involutus*, phyA1 (from aa 21; SEQ ID NO: 17; and phyA2 (from aa 21, WO 98/28409; SEQ ID NO: 18); *Trametes pubescens* (from aa 24, WO 98/28409; SEQ ID NO: 19); *Agrocybe pediades* (from aa 19, WO 98/28409; SEQ ID NO: 20); and *Peniophora lycii* (from aa 21, WO 98/28409; SEQ ID NO: 21),
30 starting with the amino acid residues mentioned in parentheses, were used for the alignment and the calculation of the

corresponding consensus sequence called "Basidio" (Example 2; SEQ ID NO: 22). The alignment was performed with the program PILEPUP. The location of the gaps was refined by hand. The consensus sequence was calculated by the program PRETTY. While a 5 vote weight of 0.5 was assigned to the two *P. involutus* phytases, all other genes were used with a vote weight of 1.0 for the consensus sequence calculation. At positions where the program was not able to determine a consensus residue, the Basidio sequence contains a dash. Capitalized amino acid 10 residues in the alignment at a given position represent the amino acid coalition that established the consensus residue.

Figure 4: Design of consensus phytase-10 amino acid sequence. By adding the sequence of *Thermomyces lanuginosus* 15 phytase [Berka, R. M., Rey, M. W., Brown, K. M., Byun, T. & Klotz, A. V. (1998) Molecular characterization and expression of a phytase gene from the thermophilic fungus *Thermomyces lanuginosus*. *Appl. Environ. Microbiol.* 64, 4423-4427; SEQ ID NO: 23] and the consensus sequence of the phytases from five 20 Basidiomycetes (SEQ ID NO: 22) to the alignment of Figure 1, an improved consensus sequence was calculated by the program PRETTY. Additionally, the amino acid sequence of *A. niger* T213 was omitted, and a vote weight of 0.5 was assigned to the remaining two *A. niger* phytase sequences. For further 25 information see Example 2.

Figure 5: DNA and amino acid sequence of consensus phytase-10 (SEQ ID NO: 25, and SEQ ID NO: 26, respectively). The amino acid sequence is written above the corresponding DNA 30 sequence using the one-letter code. The sequence of the oligonucleotides that were used to assemble the gene are in

bold letters. The names of the respective oligonucleotides and the amino acids that differ relative to consensus phytase-1 are underlined. The fcp10 gene was assembled from the following oligonucleotides: CP-1, CP-2, CP-3.10, CP-4.10, CP-5.10, CP-6, 5 CP-7.10, CP-8.10, CP-9.10, CP-10.10, CP-11.10, CP-12.10, CP-13.10, CP-14.10, CP-15.10, CP-16.10, CP-17.10, CP18.10, CP-19.10, CP-20.10, CP-21.10, and CP-22.10. The newly synthesized oligonucleotides are additionally marked by the number 10. The phytase contains the following 32 exchanges relative to 10 consensus phytase-1: Y54F, E58A, D69K, D70G, A94K, N134Q, I158V, S187A, Q188N, D197N, S204A, T214L, D220E, L234V, A238P, D246H, T251N, Y259N, E267D, E277Q, A283D, R291I, A320V, R329H, S364T, I366V, A379K, S396A, G404A, Q415E; A437G, A463E. The underlined mutations revealed a stabilizing effect on consensus phytase-1 15 when tested as single mutations in consensus phytase-1.

Figure 6: Alignment for the design of consensus phytase-11 (SEQ ID NO: 27). In contrast to the design of consensus phytase-10, for the design of the amino acid sequence of consensus 20 phytase-11, all Basidiomycete phytases were used as independent sequences using an assigned vote weight of 0.2 for each Basidiomycete sequence. Additionally, the amino acid sequence of A. niger T213 was again used in this alignment.

Figure 7: DNA and amino acid sequence of consensus phytase-1-thermo[8]-Q50T-K91A (SEQ ID NO: 28, and SEQ ID NO: 29, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to consensus phytase-1) 30 are underlined. The stop codon of the gene is marked by a star (*).

Figure 8: DNA and amino acid sequence of consensus phytase-10-thermo[3]-Q50T-K91A (SEQ ID NO: 30, and SEQ ID NO: 31, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to consensus phytase-10) are underlined. The stop codon of the gene is marked by a star (*).

Figure 9: DNA and amino acid sequence of A. fumigatus ATCC 13073 phytase alpha-mutant Q51T (SEQ ID NO: 32, and SEQ ID NO: 33, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to A. fumigatus ATCC 13073 phytase) are underlined. The stop codon of the gene is marked by a star (*).

Figure 10: DNA and amino acid sequence of consensus phytase-7 (SEQ ID NO: 34, and SEQ ID NO: 35, respectively). The amino acids are written above the corresponding DNA sequence using the one-letter code. The sequence of the oligonucleotides used to assemble the gene are in bold letters. Oligonucleotides and amino acids that were exchanged (relative to consensus phytase-1) are underlined and the corresponding triplets are written in small case letters. The fcp7 gene was assembled from the following oligonucleotides: CP-1, CP-2, CP-3, CP-4.7, CP-5.7, CP-6, CP-7, CP-8.7, CP-9, CP-10.7, CP-11.7, CP-12.7, CP-13.7, CP-14.7, CP-15.7, CP-16, CP-17.7, CP-18.7, CP-19.7, CP-20, CP-21, and CP-22. The newly synthesized oligonucleotides are additionally marked by the number 7. Consensus phytase-7 contains the following 24 exchanges in comparison to the

original consensus phytase-1: S89D, S92G, A94K, D164S, P201S, G203A, G205S, H212P, G224A, D226T, E255T, D256E, V258T, P265S, Q292H, G300K, Y305H, A314T, S364G, M365I, A397S, S398A, G404A, and A405S.

5

Figure 11: Differential scanning calorimetry (DSC) of consensus phytase-1 and consensus phytase-10. The protein samples were concentrated to about 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of consensus phytase-10 (upper graph) yielded a melting temperature of 85.4°C, which is 7.3°C higher than the melting point of consensus phytase-1 (78.1°C, lower graph).

15 Figure 12: Differential scanning calorimetry (DSC) of consensus phytase-10-thermo[3]-Q50T and consensus phytase-10-thermo[3]-Q50T-K91A. The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied 20 up to 95°C. DSC of consensus phytase-10-thermo[3]-Q50T (upper graph) yielded a melting temperature of 88.6°C, while the melting temperature of consensus phytase-10-thermo-Q50T-K91A was determined to be 89.3°C.

25 Figure 13: Comparison of the temperature optimum between consensus phytase-1, consensus phytase-10 and consensus phytase-10-thermo[3]-Q50T. For the determination of the temperature optimum, the phytase standard assay of Example 9 was performed at a series of temperatures between 37 and 86°C. The diluted 30 supernatant of transformed *S. cerevisiae* strains was used for the determination. The other components of the supernatant had

no influence on the determination of the temperature optimum: ^,
 consensus phytase-1; ◆, consensus phytase-10; ■, consensus
 phytase 10-thermo[3]-Q50T.

5 Figure 14: pH-dependent activity profile and substrate specificity of consensus phytase-10 and its variants thermo[3]-Q50T and thermo[3]-Q50T-K91A. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows the pH-
 10 dependent activity profile of consensus phytase-10 (□), consensus phytase-10-thermo[3]-Q50T (●), and consensus phytase-10-thermo[3]-Q50T-K91A (^). Graph b) shows the corresponding substrate specificity tested by replacement of phytate in the standard assay by the indicated compounds; open bars, consensus
 15 phytase-10; grey bars, consensus phytase-10-thermo[3]-Q50T; dark bars, consensus phytase-10-thermo[3]-Q50T-K91A). The numbers correspond to the following substrates: 1, phytate; 2, p-nitrophenyl phosphate; 3, phenyl phosphate; 4, fructose-1,6-bisphosphate; 5, fructose-6-phosphate; 6, glucose-6-phosphate;
 20 7, ribose-5-phosphate; 8, DL-glycerol-3-phosphate; 9, glycerol-2-phosphate; 10, 3-phosphoglycerate; 11, phosphoenolpyruvate; 12, AMP; 13, ADP; 14, ATP.

25 Figure 15: pH-dependent activity profile and substrate specificity of consensus phytase-1-thermo[8]-Q50T and of consensus phytase-1-thermo[8]-Q50T-K91A. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows the pH-
 dependent activity profile of the Q50T- (■) and the Q50T-K91A-

variant (.). Graph b) shows the corresponding substrate specificities tested by replacement of phytate in the standard assay by the indicated compounds (open bars, consensus phytase-1-thermo[8]-Q50T; filled bars, consensus phytase-1-thermo[8]-Q50T-K91A). The substrates are listed in the legend of Figure 14.

Figure 16: Differential scanning calorimetry (DSC) of consensus phytase-1-thermo[8]-Q50T and consensus phytase-1-thermo[8]-Q50T-K91A. The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of consensus phytase-1-thermo[8]-Q50T (upper graph) showed a melting temperature of 84.7°C, while the melting point of consensus phytase-1-thermo[8]-Q50T-K91A was found at 85.7°C.

Figure 17: Comparison of the temperature optimum between consensus phytase-1, consensus phytase-1-thermo[3] and consensus phytase-1-thermo[8]. For the determination of the temperature optimum, the phytase standard assay was performed at a series of temperatures between 37 and 86°C. Protein purified from the supernatant of transformed *S. cerevisiae* strains was used for the determination. O, consensus phytase-1; □, consensus phytase-1-thermo[3]; ▲, consensus phytase 1-thermo[8].

Figure 18: Comparison of the pH-dependent activity profile and substrate specificity between consensus phytase-1, consensus phytase-7, and the phytase from *A. niger* NRRL 3135. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows

the pH-dependent activity profile of consensus phytase-1 (■), the phytase from *A. niger* NRRL 3135 (○), and of consensus phytase-7 (▲). Graph b) shows the corresponding substrate specificities tested by replacement of phytate in the standard assay by the indicated compounds (black bars, *A. niger* NRRL 3135 phytase; open bars, consensus phytase-1; dashed bars, consensus phytase-7). The substrates are listed in the legend of Figure 14.

Figure 19: Differential scanning calorimetry (DSC) of the phytase from *A. fumigatus* ATCC 13073 and of its stabilized alpha-mutant, which contains the following amino acid exchanges: F55Y, V100I, F114Y, A243L, S265P, and N294D.

The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of *A. fumigatus* 13073 phytase (lower graph) revealed a melting temperature of 62.5°C, while the melting point of the alpha-mutant was found at 67.0°C.

Figure 20: Comparison of the temperature optima of *A. fumigatus* 13073 wild-type phytase, its alpha-mutant, and a further stabilized alpha-mutant (E59A-S154N-R329H-S364T-G404A). For the determination of the temperature optimum, the phytase standard assay was performed at a series of temperatures between 37 and 75°C. The diluted supernatant of transformed *S. cerevisiae* strains was used for the determination. The other components of the supernatant had no influence on the determination of the temperature optimum. ○, *A. fumigatus* ATCC 13073 phytase; ▲, *A. fumigatus* ATCC 13073 alpha-mutant; □, *A.*

fumigatus ATCC 13073 alpha-mutant- (E59A-S154N-R329H-S364T-G404A) -Q27T; ■, A. fumigatus ATCC 13073 alpha-mutant- (E59A-S154N-R329H-S364T-G404A) -Q51T-K92A. Q51T and K92A correspond to consensus phytase-1 substitutions Q50T and K91A, respectively.

5

Figure 21: Amino acid sequence of consensus phytase-12 (consphy12; SEQ ID NO: 36) which contains a number of active site residues transferred from the "basidio" consensus sequence to consensus phytase-10-thermo[3] -Q50T-K91A (underlined).

10

Figure 22: DNA and amino acid sequence of consensus phytase-3-thermo[11] -Q50T. The amino acids are written below the corresponding DNA sequence using the one-letter code.

15

Figure 23: DNA and amino acid sequence of consensus phytase-3-thermo[11] -Q50T-K91A. The amino acids are written below the corresponding DNA sequence using the one-letter code.

20

Figure 24: DNA and amino acid sequence of consensus phytase-10-thermo[5] -Q50T. The amino acids are written below the corresponding DNA sequence using the one-letter code.

25

Figure 25: DNA and amino acid sequence of consensus phytase-10-thermo[5] -Q50T-K91A. The amino acids are written below the corresponding DNA sequence using the one-letter code.

30

The phytase-producing microorganism strains mentioned herein, viz. Paxillus involutus CBS 100231; Peniophora lycii CBS 686.96; Agrocybe pediades CBS 900.96; and Trametes pubescens CBS 100232; were isolated from natural samples originating from, respectively, Denmark; Denmark; Denmark; and Sweden (the Uppsala

collection. The samples were collected in November 1992; October 1993; June 1995; and in November 1995, respectively.

Example 1

5 Consensus phytase-1

The amino acid sequence of consensus phytase-1 (fungal consensus phytase, fcp) was designed and calculated as described in Examples 1 and 2 of EP 897985. Table 1 below shows the origin and vote weight of the phytase amino acid sequences used for the 10 design of consensus phytase-1. The consensus phytase-1 sequence was furthermore converted into a DNA sequence as described in Example 3 of EP 897985, and the consensus phytase-1 gene was constructed and cloned as described in Example 4 of EP 897985.

15 Table 1

Origin and vote weight of the phytase amino acid sequences

- phyA from Aspergillus terreus 9A-1, aa 27, vote weight 0.5 (Mitchell et al., 1997)
- phyA from Aspergillus terreus cbs116.46, aa 27, vote weight 20 0.5 (EP 897985)
- phyA from Aspergillus niger var. awamori, aa 27, vote weight 0.33 [Piddington, C. S., Houston, C. S., Paloheimo, M., Cantrell, M., Miettinen-Oinonen, A., Nevalainen, H., & Rambosek, J. (1993) The cloning and sequencing of the genes encoding 25 phytase (phy) and pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var. awamori. Gene 133, 55-62].
- phyA from Aspergillus niger T213 (EP 897985), aa 27, vote weight 0.33
- 30 - phyA from Aspergillus niger strain NRRL3135, aa 27, vote weight 0.33 (van Hartingsveldt et al., 1993)

- phyA from *Aspergillus fumigatus* ATCC 13073, aa 26, vote weight 0.2 (Pasamontes et al., 1997)

- phyA from *Aspergillus fumigatus* ATCC 32722, aa 26, vote weight 0.2 (EP 897985)

5 - phyA from *Aspergillus fumigatus* ATCC 58128, aa 26, vote weight 0.2 (EP 897985)

- phyA from *Aspergillus fumigatus* ATCC 26906, aa 26, vote weight 0.2 (EP 897985)

- phyA from *Aspergillus fumigatus* ATCC 32239, aa 30, vote weight 10 0.2 (EP 897985)

- phyA from *Emericella nidulans*, aa 25, vote weight 1.0 (Pasamontes et al., 1997a)

- phyA from *Talaromyces thermophilus* ATCC 20186, aa 24, vote weight 1.0 (Pasamontes et al., 1997a)

15 - phyA from *Myceliophthora thermophila*, aa 19, vote weight 1.0 (Mitchell et al., 1997)

Example 2

Design of an improved consensus phytase (consensus
20 phytase-10) amino acid sequence

The alignments used for the design of consensus phytase-10 were calculated using the program PILEUP from the GCG Sequence Analysis Package Release 9.0 (Devereux et al., 1984) with the 25 standard parameters (gap creation penalty 12, gap extension penalty 4). The location of the gaps was refined using a text editor.

The following sequences were used for the alignment of the Basidiomycete phytases starting with the amino acid (aa) 30 mentioned in Table 2:

Table 2

Origin and vote weight of five Basidiomycete phytases used for the calculation of the corresponding consensus amino acid sequence (basidio)

5

- phyA1 from Paxillus involutus CBS No. 100231, aa 21, vote weight 0.5 (WO 98/28409)
- phyA2 from Paxillus involutus CBS No. 100231, aa 21, vote weight 0.5 (WO 98/28409)
- 10 - phyA from Trametes pubescens CBS No. 100232, aa 24, vote weight 1.0 (WO 98/28409)
- phyA from Agrocybe pediades CBS No. 900.96, aa 19, vote weight 1.0 (WO 98/28409)
- phyA from Peniophora lycii CBS No. 686.96, aa 21, vote weight 15 1.0 (WO 98/28409)

The alignment is shown in Figure 3.

In Table 3 the genes that were used for the final alignment are listed. The first amino acid (aa) of the sequence that is used in the alignment is mentioned behind the organism's designation.

Table 3

25 Origin and vote weight of the phytase sequences used for the design of consensus phytase-10

- phyA from Aspergillus terreus 9A-1, aa 27, vote weight 0.5 (Mitchell et al., 1997)
- 30 - phyA from Aspergillus terreus cbs116.46, aa 27, vote weight 0.5 (EP 897985)

- phyA from *Aspergillus niger* var. *awamori*, aa 27, vote weight 0.5 (Piddington et al., 1993)
- phyA from *Aspergillus niger* strain NRRL3135, aa 27, vote weight 0.5 (van Hartingsveldt et al., 1993)
- 5 - phyA from *Aspergillus fumigatus* ATCC 13073, aa 26, vote weight 0.2 (Pasamontes et al., 1997)
- phyA from *Aspergillus fumigatus* ATCC 32722, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 58128, aa 26, vote weight 10 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 26906, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 32239, aa 30, vote weight 0.2 (EP 897985)
- 15 - phyA from *Emericella nidulans*, aa 25, vote weight 1.0 (Pasamontes et al., 1997a)
- phyA from *Talaromyces thermophilus* ATCC 20186, aa 24, vote weight 1.0 (Pasamontes et al., 1997a)
- phyA from *Myceliophthora thermophila*, aa 19, vote weight 1.0 20 (Mitchell et al., 1997)
- phyA from *Thermomyces lanuginosus*, aa 36, vote weight 1.0 (Berka et al., 1998)
- Consensus sequence of five Basidiomycete phytases, vote weight 1.0 (Basidio, Figure 3)

25

The corresponding alignment is shown in Figure 4.

Calculation of the amino acid sequence of consensus phytase-10

30 To improve the alignment, we added the original consensus sequence of five phytases from four different Basidiomycetes

(called Basidio; still containing the undefined sequence positions; see Figure 3), nearly all phytase sequences used for the calculation of the original consensus phytase sequences and one new phytase sequence from the Ascomycete *Thermomyces lanuginosus* to a larger alignment.

We set plurality on 2.0 and threshold on 3. The used vote weights are listed in Table 3. The alignment and the corresponding consensus sequence are presented in Figure 4. The new consensus phytase sequence has 32 different amino acids in comparison to the original consensus phytase-1. Positions for which the program PRETTY was not able to calculate a consensus amino acid residue were filled according to rules mentioned in Example 1. None of the residues suggested by the program was replaced.

Furthermore, in another calculation, we included all Basidiomycete phytases as single amino acid sequences but assigning a vote weight of 0.2 in the calculation. The corresponding alignment is shown in Figure 6. The calculated consensus amino acid sequence (consensus phytase-11) has the following differences to the sequence of consensus phytase-10. Letter X means that the program was not able to calculate a consensus amino acid; the amino acid in parenthesis corresponds to the amino acid finally included into consensus phytase-10.

D35X (first letter for consensus phytase-10, last letter for consensus phytase-11), X(K)69K, X(E)100E, A101R, Q134N, X(K)153N, X(H)190H, X(A)204S, X(E)220D, E222T, V227A, X(R)271R, H287A, X(D)288D, X(K)379K, X(I)389I, E390X, X(E)415E, X(A)416A, X(R)446L, E463A. The numbering is as in Fig. 5.

We also checked single amino acid replacements suggested by the improved consensus sequences 10 and 11 on their influence

on the stability of the original consensus phytase-1. The approach is described in example 3.

Conversion of the consensus phytase-10 amino acid sequence
5 into a DNA sequence

The first 26 amino acid residues of *A. terreus* cbs116.46 phytase were used as signal peptide and fused to the N-terminus of consensus phytase-10. The used procedure is further described in Example 1.

10 The resulting sequence of the fcp10 gene is shown in Figure 5.

Construction and cloning of the consensus phytase-10 gene
(fcp10)

15 The calculated DNA sequence of fcp10 was divided into oligonucleotides of 85 bp, alternately using the sequence of the sense and the anti-sense strand. Every oligonucleotide overlaps 20 bp with the previous and the following oligonucleotide of the opposite strand. The location of all primers, purchased from
20 Microsynth, Balgach (Switzerland) and obtained in a PAGE-purified form, is indicated in Figure 5.

PCR-Reactions

In three PCR reactions, the synthesized oligonucleotides
25 were composed to the entire gene. For the PCR, the High Fidelity Kit from Boehringer Mannheim (Boehringer Mannheim, Mannheim, Germany) and the thermo cycler "The ProtokolTM" from AMS Biotechnology (Europe) Ltd. (Lugano, Switzerland) were used. The following oligonucleotides were used in a concentration of 0.2
30 pMol/ml.

Mix 1.10: CP-1, CP-2, CP-3.10, CP-4.10, CP-5.10, CP-6,
CP-7.10, CP-8.10, CP-9.10, CP-10.10

Mix 2.10: CP-9.10, CP-11.10, CP-12.10, CP-13.10, CP-
5 14.10, CP-15.10, CP-16.10, CP-17.10, CP-18.10,
CP-19.10, CP-20.10, CP-21.10, CP-22.10

The newly synthesized oligonucleotides are marked by the
number 10. Consensus phytase-10 contains the following 32
exchanges, which are underlined in Figure 5, in comparison to
10 the original consensus phytase-1: Y54F, E58A, D69K, D70G, A94K,
N134Q, I158V, S187A, Q188N, D197N, S204A, T214L, D220E, L234V,
A238P, D246H, T251N, Y259N, E267D, E277Q, A283D, R291I, A320V,
R329H, S364T, I366V, A379K, S396A, G404A, Q415E, A437G, A463E.

Four short PCR primers were used for the assembling of the
15 oligonucleotides:

CP-a: *Eco RI*
5' -TATATGAATTCATGGCGTGTCGTC-3' (SEQ ID NO: 37)

20 CP-b:
5' -TGAAAAGTTCATTGAAGGTTTC-3' (SEQ ID NO: 38)

CP-c.10:
5' -TCTTCGAAAGCAGTACACAAAC-3' (SEQ ID NO: 39)

25 CP-e: *Eco RI*
5' -TATATGAATTCTTAAGCGAAC-3' (SEQ ID NO: 40)

PCR reaction a: 10 μ l Mix 1.10 (2.0 pmol of each oligonucleotide)

2 μ l nucleotides (10 mM of each nucleotide)

2 μ l primer CP-a (10 pmol/ml)

5 2 μ l primer CP-c.10 (10 pmol/ml)

10,0 μ l PCR buffer

0.75 μ l polymerase mixture (2.6 U)

73.25 μ l H₂O

10 PCR reaction b: 10 μ l Mix 2.10 (2.0 pmol of each oligonucleotide)

2 μ l nucleotides (10 mM each nucleotide)

2 μ l primer CP-b (10 pmol/ml)

2 μ l primer CP-e (10 pmol/ml)

15 10,0 μ l PCR buffer

0.75 μ l polymerase mixture (2.6 U)

73.25 μ l H₂O

Reaction conditions for PCR reactions a and b:

20 step 1 2 min - 45°C

step 2 30 sec - 72°C

step 3 30 sec - 94°C

step 4 30 sec - 52°C

step 5 1 min - 72°C

25

Steps 3 to 5 were repeated 40-times.

The PCR products (670 and 905 bp) were purified by agarose gel electrophoresis (0.9% agarose), followed by gel extraction 30 (QIAEX II Gel Extraction Kit, Qiagen, Hilden, Germany). The purified DNA fragments were used for the PCR reaction c.

PCR reaction c: 6 µl PCR product of reaction a ≈50 ng)
 6 µl PCR product of reaction b ≈50 ng)
 2 µl primer CP-a (10 pmol/ml)
5 2 µl primer CP-e (10 pmol/ml)
 10,0 µl PCR buffer
 0.75 µl polymerase mixture (2.6 U)
 73.25 µl H₂O

10 Reaction conditions for PCR reaction c:

step 1 2 min - 94°C
step 2 30 sec - 94°C
step 3 30 sec - 55°C
step 4 1 min - 72°C

15

Steps 2 to 4 were repeated 31-times.

The resulting PCR product (1.4 kb) was purified as mentioned above, digested with EcoRI, and ligated in an EcoRI-digested and dephosphorylated pBsk(-)-vector (Stratagene, La Jolla, CA, USA). 1 µl of the ligation mixture was used to transform E. coli XL-1 competent cells (Stratagene, La Jolla, CA, USA). All standard procedures were carried out as described by Sambrook et al. (1987). The DNA sequence of the constructed gene (fcp10) was checked by sequencing as known in the art.
25

Example 3

Increasing the thermostability of consensus phytase-1 by introduction of single mutations suggested by the amino acid sequences of consensus phytase-10 and consensus phytase-11

5

In order to increase the thermostability of homologous genes, it is also possible to test the stability effect of each differing amino acid residue between the protein of interest and 10 the calculated consensus sequence and to combine all stabilizing mutations into the protein of interest. We used the consensus phytase-1 as protein of interest and tested the effect on the protein stability of 34 amino acid residues that differ relative to consensus phytase-10 and/or -11 by single site-directed 15 mutagenesis.

To construct muteins for expression in *A. niger*, *S. cerevisiae*, or *H. polymorpha*, the corresponding expression plasmid containing the consensus phytase-1 gene was used as template for site-directed mutagenesis (see Examples 6-8). 20 Mutations were introduced using the "quick exchange™ site-directed mutagenesis kit" from Stratagene (La Jolla, CA, USA) following the manufacturer's protocol and using the corresponding primers. All mutations made and the corresponding primers are summarized in Table 4. Plasmids harboring the 25 desired mutation were identified by DNA sequence analysis as known in the art.

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Table 4

Primers used for site-directed mutagenesis of consensus phytase-1

Exchanged bases are highlighted in bold. The introduction of a restriction site is marked above the sequence. When a restriction site is written in parenthesis, the mentioned site was destroyed by introduction of the mutation.

mutation Primer set

| | | |
|----|-------|--|
| 10 | | <i>Kpn I</i> |
| | Q50T | 5' - CACTTG TGGGGT A CTACTCTCCATACTTCTC-3' (SEQ ID NO: 41) 5' - GAGAAGTATGGAGAGT AGGT ACCCCACAAGTG-3' |
| 15 | Y54F | 5' - GGTCAAA T ACTCTCCATTCTCTCTGGAAAG-3' (SEQ ID NO: 42) 5' - CTTCCAAAGAGAAG A ATGGAGAGTATTGACC-3' |
| | E58A | 5' - CATACTTCTCTTGG C AGACGAATCTGC-3' (SEQ ID NO: 43) 5' - GCAGATT CGT T GCCAAAGAGAAGTATG-3' |
| 20 | | <i>Aat II</i> |
| | D69K | 5' - CTCCAGACGT CCC AAAGGACTGTAGAGTTAC-3' (SEQ ID NO: 44) 5' - GTAACTCTACAG CCG TCTGG GAC GTCTGGAG-3' |
| 25 | D70G | <i>Aat II</i> |
| | | 5' - CTCCAGACGT CCC AGACGG G CTGTAGAGTTAC-3' (SEQ ID NO: 45) 5' - GTAACTCTACAG CCG TCTGG GAC GTCTGGAG-3' |
| | K91A | 5' - GATA CC AACTTCTT GCG TCTAAGGCTTACTCTG-3' (SEQ ID NO: 46) |
| 30 | | 5' - CAGAGTAAGCCTTAGAC G CAGAAGAAGTTGGGTATC-3' |
| | | <i>Sca I</i> |
| | A94K | 5' - CTTCTAAGTCTAAG AAG TACTCTGCTTG-3' (SEQ ID NO: 47) 5' - CAAAGCAGAGT ACTT CTTAGACTT AAG -3' |
| 35 | A101R | 5' - GCTTACTCTGCTTGATTGAACGGATTCAAAGAACGCTAC-3' (SEQ ID NO: 48) 5' - GTAGCGTTCTTGAAT CCG TCAATCAAAGCAGAGTAA GC -3' |
| 40 | N134Q | 5' - CCATTCGGTGAACAGCAAATGGTTAACTC-3' (SEQ ID NO: 49) 5' - GAGTTAACCATTG C TGTTCACCGAATGG-3' |

| | | |
|----|-------|--|
| | | <i>Nru</i> I |
| 10 | K153N | 5' -GATACAAGGCT CTCGCGAGAACATTGTTC -3' (SEQ ID NO: 50) 5' -GGAACAAT GTTCTCGCGAGAGCCTGTATC -3' |
| 15 | I158V | <i>Bss</i> HI |
| | | 5' -GATTGTTCCATT CGTGC CGCTCTGGTTC-3' (SEQ ID NO: 51) 5' -GAACCAGAAG CGCGCACGA ATGGAACAATC-3' |
| 20 | S187A | <i>Apa</i> I |
| | | 5' -GGCTGACCCAGGG GCC CAACCACACCAAGC-3' (SEQ ID NO: 53) 5' -GCTTGGTGTGGTT GGGCC CCTGGGTAGCC-3' |
| 25 | D197N | <i>Bcl</i> I |
| | | 5' -CTCCAGTTATT AACGTGATC ATTCCAGAAGG-3' (SEQ ID NO: 52) 5' -CCTTCTGGAAT GATCACGT TAATAACTGGAG-3' |
| 30 | T214L | <i>Nco</i> I |
| | | 5' -CACTTGACCAT GGTCTTGT ACTGCTTCG-3' (SEQ ID NO: 54) 5' -CGAAAGCAGTACAAAG ACCA TGGTCAAAGTG-3' |
| 35 | E222T | <i>Avr</i> II |
| | | 5' -GCTTTCGAAGACT CTACCC TAGGTGACGACGTTG-3' (SEQ ID NO: 55) |
| | V227A | 5' -CACAGTCGTAC CTAGGG TAGAGTCTCGAAAGC-3' |
| 40 | L234V | <i>Sac</i> II |
| | | 5' -CTAACTTC ACCGCGG TGTTCGCTCCAG-3' (SEQ ID NO: 57) 5' -CTGGAGCGAAC ACCGCGG TGAAGTTAG-3' |
| 45 | A238P | 5' -GCTTGTTCGCTCC ACCTATTAG AGCTAGATTGG-3' (SEQ ID NO: 58) |
| | | 5' -CCAATCTAGCTCTAACAG TTAAC GGAGCGAACAAAGC-3' |
| 50 | T251N | <i>Hpa</i> I |
| | | 5' -GCCAGGT TTAAC TTG ACTG ACGAAG-3' (SEQ ID NO: 59) 5' -TTCGTCAGT CAAG TTAACAC CTGGC -3' |
| 55 | Y259N | <i>Aat</i> II |
| | | 5' -GACGAAG ACGT CGTT AACTT GATGGAC-3' (SEQ ID NO: 60) 5' -GTCCAT CAAG TTAAC CGAC GTCTCGTC-3' |
| 60 | E267D | <i>Asp</i> I |
| | | 5' -GTCCATT CGAC ACT GT CGCTAGAAC TTC -3' (SEQ ID NO: 61) 5' -GAAGTT CTAG CGACAG GT CGAATGGAC-3' |

E277Q 5' - CTGACGCTACTCAGCTGTCTCCATTC-3' (SEQ ID NO: 62)
 5' - GAATGGAGACAGCTGAGTAGCGTCAG-3'

5 A283D 5' - GTCTCCATTCTGTG**ATTTGTT**CACTCAC-3' (SEQ ID NO: 63)
 5' - GTGAGTGAA**CAAAT**CACAGAATGGAGAC-3'

Ksp I

H287A 5' - GCTTTGTTCAC**CCGCG**GACGAATGGAG-3' (SEQ ID NO: 64)
 10 5' - CTCCATT~~CGT~~**CCGCG**GTGAACAAAGC-3'

Bam HI

R291I 5' - CACGACGAATGG**ATCCA**TACGACTAC-3' (SEQ ID NO: 65)
 15 5' - GTAGTCGTATT**GGATCC**ATT~~CGT~~CGTG-3'

Bsi WI

Q292A 5' - GACGAATGGAGA**GCGTAC**GACTACTTG-3' (SEQ ID NO: 66)
 20 5' - CAAGTAGTC**GTACG**CTCTCCATT~~CGT~~-3'

Hpa I

A320V 5' - GGTGTTGGTTTC**GTTAAC**GAATTGATTGC-3' (SEQ ID NO: 67)
 25 5' - GCAATCAATT~~CGT~~**TAAC**GAACCAACACC-3'

(*Bgl II*)

R329H 5' - GCTAGATTGACT**CAC**TCTCCAGTTCAAG-3' (SEQ ID NO: 68)
 30 5' - CTTGA~~ACTGGAGAG~~**TGAG**TCAATCTAGC-3'

Eco RV

S364T 5' - CTCACGACAAC**ACTATGATA**TCTATTTCTTC-3' (SEQ ID NO: 69)
 35 5' - GAAGAAAATAG**ATATCATAGT**GTTGTCGTGAG-3'

Nco I

I366V 5' - CGACA~~ACTCC~~**ATGG**TTCTATTTC~~TT~~CGC-3' (SEQ ID NO: 70)
 40 5' - GCGAAGAAAATAGAA**ACCATGG**AGTTGTCG-3'

Kpn I

A379K 5' - GTACAACGGT**ACCAAG**CCATTGTCTAC-3' (SEQ ID NO: 71)
 45 5' - GTAGACAATGG**CTTGG**TACCGTTGTAC-3'

S396A 5' - CTGACGGTTACGCTGCTTCTGGAC-3' (SEQ ID NO: 72)
 5' - GTCCAAGAAGCAGCGTAACCGTCAG-3'

G404A 5' - CTGTTCCATT~~CG~~GCTGCTAGAGCTTAC-3' (SEQ ID NO: 73)
 5' - GTAAGCTCTAGCAG**CGAATG**GAACAG-3'

Q415E 5' - GATGCAATGT**GAAG**CTGAAAAGGAACC-3' (SEQ ID NO: 74)
 5' - GGTTCC~~TTT~~CAG**CTTCA**CATTGCATC-3'

Sal I

A437G 5' -CACGGTTGTGGTGT**C**GACAAGTTGGG-3' (SEQ ID NO: 75)
 5' -CCCAACTTGT**C**GACACCACAACCGTG-3'

5

Mun I

A463E 5' -GATCTGGTGG**CAATT**GGGA**GG**GAATGTTTCG-3' (SEQ ID NO: 76)
 5' -CGAACACATTCC**CTCCC****AATT**GCCACCAGATC-3'

10 and, accordingly, for other mutations.

The temperature optimum of the purified phytases, expressed in *Saccharomyces cerevisiae* (Example 7), was determined as outlined in Example 9. Table 5 shows the effect of 15 each mutation introduced on the stability of consensus phytase-1.

Table 5

Stability effect of the individual amino acid replacements in
 20 consensus phytase-1

+ or - means a positive, respectively, negative effect on the protein stability up to 1°C, ++ and -- means a positive, respectively, negative effect on the protein stability between 1 and 3°C; the numbers 10 or 11 in parentheses indicate the 25 consensus phytase sequence that suggested the amino acid replacement.

| stabilizing | | neutral | | destabilizing | |
|-------------|--------|------------|-------------|---------------|--------|
| mutation | effect | mutation | ef- fect | mutation | effect |
| E58A (10) | + | D69A | ± | Y54F (10) | - |
| D69K (11) | + | D70G (10) | ± | V73I | - |
| D197N (10) | + | N134Q (10) | ± | A94K (10) | - |
| T214L (10) | ++ | G186H | ± | A101R (11) | - |
| E222T (11) | ++ | S187A (10) | ± | K153N (11) | - |
| E267D (10) | + | T214V | ± | I158V (10) | -- |
| R291I | + | T251N (10) | ± | G203A | -- |
| R329H (10) | + | Y259N (10) | ± | G205S | - |
| S364T (10) | ++ | A283D (10) | ± | A217V | - |
| A379K (11) | + | A320V (10) | ± | V227A (11) | -- |
| G404A (10) | ++ | K445T | ± | L234V (10) | - |
| | | A463E (10) | ± | A238P (10) | -- |
| | | | | E277Q (10) | - |
| | | | | H287A (11) | - |
| | | | | Q292A | - |
| | | | | I366V (10) | - |
| | | | | S396A (10) | -- |
| | | | | Q415E (11) | - |
| | | | | A437G (10) | -- |
| | | | | E451R | -- |

We combined eight positive mutations (E58A, D197N, E267D, R291I, R329H, S364T, A379K, G404A) in consensus phytase-1 thermo[8], using the primers and the technique mentioned above in this example. Furthermore, the mutations Q50T and/or K91A were introduced which mainly influence the catalytic characteristics of phytase (see patent applications EP 897010 and EP 897985, as well as Example 9). The DNA and amino acid sequence of the resulting phytase (consensus phytase-1-thermo[8]-Q50T-K91A) are shown in Figure 7. In this way, the temperature optimum and the melting point of the consensus phytase were increased by 7°C (Figures 15, 16, 17).

In a further consensus protein, we combined eleven positive mutations (E58A, D69K, D197N, T214L, E222T, E267D, R291I, R329H, S364T, A379K, G404A) in consensus phytase-1 thermo[11]. Furthermore, the mutations Q50T and/or K91A were

introduced. In this way, the melting temperature was increased by another 3-4°C when compared to consensus phytase-1 thermo[8].

Using the results of Table 5, we further improved the thermostability of consensus phytase-10 by the back mutations K94A, V158I, and A396S, the reverse of which (A94K, I158V, and S396A) revealed a strong negative influence on the stability of consensus phytase-1. The resulting protein was called consensus phytase-10-thermo[3]. SEQ ID NO: 26 plus the three mutations K94A, V158I, and A396S. Furthermore, we introduced the mutations Q50T and K91A that mainly influence the catalytic characteristics of consensus phytase (see patent applications EP 897010 and EP 897985, as well as Example 9 and Figures 14 and 15). The resulting DNA and amino acid sequence are shown in Figure 8. The optimized phytase showed a 4°C higher temperature optimum and melting point than consensus phytase-10 (Figures 12 and 13). Furthermore, the phytase has also a strongly increased specific activity with phytate as substrate of 250 U/mg at pH 5.5 (Figure 14).

In a still further consensus protein, two additional mutations were introduced into consensus phytase-10 thermo[3] (E222T, G437A) which yielded consensus phytase-10 thermo[5]. Furthermore, the mutations Q50T and/or K91A were introduced. In this way, the melting temperature was increased by another 1-2°C when compared to consensus phytase-10 thermo[3].

Example 4Stabilization of the phytase of A. fumigatus ATCC 13073 by replacement of amino acid residues with the corresponding consensus phytase-1 and/or consensus phytase-10 residues

5

At six amino acid sequence positions where A. fumigatus 13073 phytase is the only or nearly the only phytase in the alignment of Figure 1 that does not contain the corresponding consensus phytase amino acid residue, the non-consensus amino acid residue was replaced by the consensus one. The following amino acids were substituted in A. fumigatus 13073 phytase, containing additionally the Q51(24)T substitution (influencing the catalytic properties and corresponding to the Q50T substitution in the consensus phytases) and the signal sequence 15 of A. terreus CBS116.46 phytase (see European Patent Application No. 0897010, and Figure 9): F55(28)Y, V100(73)I, F114(87)Y, A243(220)L, S265(242)P, N294(282)D. The numbers in parentheses refer to the numbering in Figure 1.

In a second round, four of the seven stabilizing amino acid exchanges (E58A, R329H, S364T, G404A) identified in consensus phytase-10 and tested as single mutations in consensus phytase-1 (Table 5) were additionally introduced into the A. fumigatus alpha-mutant. Furthermore, the amino acid replacement S154N, shown to reduce the protease susceptibility of the 25 phytase, was introduced.

The mutations were introduced as described in Example 3 (see Table 6) and expressed as described in Examples 6 to 8. The resulting A. fumigatus 13073 phytase variants were called alpha-mutant (i.e. the A. fumigatus ATCC 13073 phytase with the 30 substitutions Q24T, F28Y, V73I, F87Y, A220L, S242P, N282D) and "optimized" alpha-mutant (i.e. the A. fumigatus alpha-mutant

having the additional substitutions E59A-S154N-R329H-S364T-G404A). K92A is an additional preferred mutation.

The temperature optimum (60°C, Figure 20) and the melting temperature (67.0°C, Figure 19) of the A. fumigatus 13073 alpha-5 mutant phytase were increased by 5-7°C in comparison to the values of the wild-type phytase (temperature optimum: 55°C, Tm: 60°C). The five additional amino acid replacements further increased the temperature optimum by 3°C (Figure 20).

10 Table 6

Mutagenesis primers for the stabilization of A. fumigatus ATCC 13073 phytase

| Mutation | Primer |
|----------|--|
| 15 F55Y | 5' -CACGTACTCGCC A TACTTTCGCTCGAG-3' (SEQ ID NO: 77) 5' -CTCGAGCGAAA AGTATGGCGAGTACGTG -3' |
| 20 E58A | (Xho I) 5' -CCATACTTTCGCT C GGACGAGCTGTCCGTG-3' 5' -CACGGACAGCTCG T CGAGCGAAA AGTAGG -3' |
| 25 V100I | 5' -GTATAAGAAGCTT ATT ACGGCGATCCAGGCC-3' 5' -GGCCTGGATCGCCGT A TA A GGCTTCTTATAC-3' |
| 30 F114Y | 5' -CTTCAAGGG CAAGTAC GCCTTTGAAGACG-3' 5' -CGTC TTCAAAAGGCGTACTTGCC CTTGAAG-3' |
| 35 A243L | 5' -CATCCGAGCTCG C TCGAGAAGCATCTTC-3' (SEQ ID NO: 81) 5' -GAAGATGCTT CTCGAGGCGAGCTCGGATG -3' |
| S265P | 5' -CTAATGGA TGTGT CCGTTT GATA CGGTAG -3' (SEQ ID NO: 82) 5' -CTACCGTATCAA ACGGACACATGTCCATTAG -3' |
| N294D | 5' -GTGGAAGAAGT ACGACTAC CTTCAGTC-3' (SEQ ID NO: 83) 5' -GACTGAAGGTAG TCGTACTT CCAC-3' |

(Mlu I)

R329H 5' -GCCCGGTTGACGC**A**TTCGCCAGTGCAGG-3' (SEQ ID NO: 84)
 5' -CCTGCACTGGCGA**A**TGCGTCAACCGGGC-3'

Nco I

S364T 5' -CACACGACAAC**A**C**C**CATGGTTCCATCTTC-3' (SEQ ID NO: 85)
 5' -GAAGATGGAAACC**A**CATGGTGTGTCGTGTG-3'

(Bss HI)

G404A 5' -GTGGTGCCTTCG**C****C**CGCGAGCCTACTTC-3' (SEQ ID NO: 86)
 5' -GAAGTAGGCTCG**C****G**CGAAAGGCACCAC-3'

Example 5Introduction of the active site amino acid residues of A. niger NRRL 3135 phytase into consensus phytase-1

We used the crystal structure of Aspergillus niger NRRL 3135 phytase to define all active site amino acid residues (see Example 1, and EP 897010). Using the alignment of Figure 1, we replaced the following active site residues and additionally 20 the non-identical adjacent ones of consensus phytase-1 by those of A. niger phytase:

S89D, S92G, A94K, D164S, P201S, G203A, G205S, H212P, G224A, D226T, E255T, D256E, V258T, P265S, Q292H, G300K, Y305H, A314T, S364G, M365I, A397S, S398A, G404A, and A405S.

The new consensus phytase-7 protein sequence was backtranslated into a DNA sequence (Figure 10) as described in Example 1. The corresponding gene (fcp7) was generated as described in Example 1 using the following oligonucleotide mixes:

Mix 1.7: CP-1, CP-2, CP-3, CP-4.7, CP-5.7, CP-6, CP-7, CP-8.7, CP-9, CP-10.7

Mix 2.7: CP-9, CP-10.7, CP-11.7, CP-12.7, CP-13.7, CP-14.7, CP-15.7, CP-16, CP-17.7, CP-18.7, CP-19.7, CP-20, CP-21, CP-22.

The DNA sequences of the oligonucleotides are indicated in Figure 10. The newly synthesized oligonucleotides are additionally marked by the number 7. After assembling of the 5 oligonucleotides using the same PCR primers as mentioned in Example 1, the gene was cloned into an expression vector as described in Examples 6-8.

The pH-profile of the enzyme determined after expression in *H. polymorpha* and purification was very similar to that of *A. niger* phytase (see Figure 18).

Example 6

Expression of the consensus phytase genes in Hansenula polymorpha

15 The phytase expression vectors used to transform *H. polymorpha* RB11 [Gellissen, G., Hollenberg, C. P., Janowicz, Z. A. (1994) Gene expression in methylotrophic yeasts, in Smith, A. (ed.) Gene expression in recombinant microorganisms. Dekker, New York, pp. 395-439] were constructed by inserting the Eco RI fragment 20 of pBsk-fcp or variants thereof into the multiple cloning site of the *H. polymorpha* expression vector pFPMT121, which is based on an ura3 selection marker from *S. cerevisiae*, a formate dehydrogenase (FMD) promoter element and a methanol oxidase (MO) terminator element from *H. polymorpha*. The 5' end of the fcp 25 gene is fused to the FMD promoter, the 3' end to the MOX terminator (Gellissen et al., Appl. Microbiol. Biotechnol. 46, 46-54, 1996; EP 299108). The resulting expression vectors are designated pFPMTfcp, pFPMTfcp10, and pFPMTfcp7.

The constructed plasmids were propagated in *E. coli*. 30 Plasmid DNA was purified using standard state of the art procedures. The expression plasmids were transformed into the *H.*

polymorpha strain RB11 deficient in orotidine-5'-phosphate decarboxylase (ura3) using the procedure for preparation of competent cells and for transformation of yeast as described in Gellissen et al. (1996). Each transformation mixture was plated 5 on YNB medium (0.14% w/v Difco YNB and 0.5% ammonium sulfate) containing 2% glucose and 1.8% agar, and incubated at 37 °C. After 4 to 5 days individual transformant colonies were picked and grown in the liquid medium described above for 2 days at 37 °C. Subsequently, an aliquot of this culture was used to 10 inoculate fresh vials with YNB-medium containing 2% glucose. After seven further passages in selective medium, the expression vector had integrated into the yeast genome in multimeric form. Subsequently, mitotically stable transformants were obtained by two additional cultivation steps in 3 ml non-selective liquid 15 medium (YPD, 2% glucose, 10 g/l yeast extract, and 20 g/l peptone). In order to obtain genetically homogeneous recombinant strains, an aliquot from the last stabilization culture was plated on a selective plate. Single colonies were isolated for analysis of phytase expression in YNB containing 2% glycerol 20 instead of glucose to derepress the FMD promoter. Purification of the consensus phytases was done as described in Example 7.

Example 7

Expression of the consensus phytase genes in *Saccharomyces* 25 *cerevisiae* and purification of the phytases from the culture supernatant

The consensus phytase genes were isolated from the corresponding Bluescript-plasmid (pBsk-fcp, pBSK-fcp10, pBsk- 30 fcp7) and ligated into the Eco RI sites of the expression cassette of the *Saccharomyces cerevisiae* expression vector pYES2

(Invitrogen, San Diego, CA, USA) or subcloned between the shortened GAPFL (glyceraldehyde-3-phosphate dehydrogenase) promoter and the pho5 terminator as described by Janes et al., Curr. Genet. 18, 97-103. The correct orientation of the gene was checked by PCR. Transformation of *S. cerevisiae* strains, e.g. INVSc1 (Invitrogen, San Diego, CA, USA), was done according to Hinnen et al., Proc. Natl. Acad. Sci. USA 75, 1929-1933 (1978). Single colonies harboring the phytase gene under the control of the GAPFL promoter were picked and cultivated in 5 ml selection medium [SD-uracil; Sherman, J. P., Finck, G. R. & Hicks, J. B. (1986) Laboratory course manual for methods in yeast genetics. Cold Spring Harbor University] at 30°C under vigorous shaking (250 rpm) for one day. The preculture was then added to 500 ml YPD medium (Sherman et al., 1986) and grown under the same conditions. Induction of the gal1 promoter was done according to the manufacturer's instructions. After four days of incubation, the cell broth was centrifuged (7000 rpm, GS3 rotor, 15 min, 5°C) to remove the cells, and the supernatant was concentrated by way of ultrafiltration in Amicon 8400 cells (PM30 membranes; Grace AG, Wallizeller, Switzerland) and ultrafree-15 centrifugal filter devices (Biomax-30K, Millipore, Bedford, MA, USA). The concentrate (10 ml) was desalted on a 40 ml Sephadex G25 Superfine column (Pharmacia Biotech, Freiburg, Germany), with 10 mM sodium acetate, pH 5.0, serving as elution buffer. The desalted sample was brought to 2 M $(\text{NH}_4)_2\text{SO}_4$ and directly loaded onto a 1 ml Butyl Sepharose 4 Fast Flow hydrophobic interaction chromatography column (Pharmacia Biotech, Feiburg, Germany) which was eluted with a linear gradient from 2 M to 0 M $(\text{NH}_4)_2\text{SO}_4$ in 10 mM sodium acetate, pH 5.0. Phytase was eluted in the breakthrough, concentrated and loaded on a 120 ml Sephadryl S-300 gel permeation chromatography column (Pharmacia Biotech,

Freiburg, Germany). Consensus phytases -1, -7 and -10 eluted as a homogeneous symmetrical peak and were shown by SDS-PAGE to be approx. 95% pure.

5 Example 8Expression of the consensus phytase genes in Aspergillus niger

The Bluescript-plasmids pBsk-fcp, pBsk-fcp10, and pBsk-fcp7 were used as template for the introduction of a Bsp HI-site upstream of the start codon of the genes and an Eco RV-site downstream of the stop codon. The ExpandTM High Fidelity PCR Kit (Boehringer Mannheim, Mannheim, Germany) was used with the following primers:

15 Primer Asp-1:

Bsp HI

5'-TATATCATGAGCGTGGTCGTGCTACTGTTC-3' (SEQ ID NO: 87)

Primer Asp-2 used for cloning of fcp and fcp7:

20

Eco RV

3'-ACCCGACTTACAAAGCGAATTCTATAGATATAT-5' (SEQ ID NO: 88)

Primer Asp-3 used for cloning of fcp10:

25

Eco RV

3'-ACCCTTCTTACAAAGCGAATTCTATAGATATAT-5' (SEQ ID NO: 89)

The reaction was performed as described by the supplier.

30 The PCR-amplified fcp-genes had a new Bsp HI site at the start codon, introduced by primer Asp-1, which resulted in a

replacement of the second amino acid residue glycine by serine. Subsequently, the DNA-fragment was digested with Bsp HI and Eco RV and ligated into the Nco I site downstream of the glucoamylase promoter of *Aspergillus niger* (*glaA*) and the Eco RV site upstream of the *Aspergillus nidulans* tryptophan C terminator (*trpC*) (Mullaney et al., 1985). After this cloning step, the genes were sequenced to detect possible errors introduced by PCR. The resulting expression plasmids, which basically correspond to the pGLAC vector as described in Example 9 of EP 684313, contained the orotidine-5'-phosphate decarboxylase gene (*pyr4*) of *Neurospora crassa* as a selection marker. Transformation of *Aspergillus niger* and expression of the consensus phytase genes was done as described in EP 684313. The consensus phytases were purified as described in Example 7.

15

Example 9

Determination of phytase activity and of the pH and temperature optima

This example relates i.a. to the determination of phytase activity and of the temperature optimum. Various phytases have been tested.

The phytase of *Aspergillus niger* NRRL 3135 was prepared as described in EP 420358 and by van Hartingsveldt et al. (Gene 127, 87-94, 1993).

25 The phytases of *Aspergillus fumigatus* ATCC 13073, *Aspergillus terreus* 9A-1, *Aspergillus terreus* cbs116.46, *Emericella nidulans*, *Myceliophthora thermophila*, and *Talaromyces thermophilus* were prepared as described in EP-0897985 and in the references therein.

30 The remaining phytases tested were prepared as described herein.

Consensus phytase-1-thermo(8) designates a variant of consensus phytase-1, which further comprises the eight mutations which are underlined in the legend to Figure 5. Consensus phytase-1 is shown in Fig. 1 (SEQ ID NO: 14) without signal peptide, and in Fig. 2 (SEQ ID NO: 16) with the signal peptide.

Phytase activity was determined basically as described by Mitchell et al. (1997). The activity was measured in an assay mixture containing 0.5% phytic acid (\approx 5 mM) in 200 mM sodium acetate, pH 5.0. After 15 min of incubation at 37°C, the reaction was stopped by addition of an equal volume of 15% trichloroacetic acid. The liberated inorganic phosphate was quantified by mixing 100 μ l of the assay mixture with 900 μ l H₂O and 1 ml of 0.6 M H₂SO₄, 2% ascorbic acid and 0.5% ammonium molybdate. Standard solutions of potassium phosphate were used as reference. One unit of enzyme activity was defined as the amount of enzyme that releases 1 μ mol phosphate per minute at 37°C. The protein concentration was determined using the enzyme extinction coefficient at 280 nm calculated according to Pace et al. [Pace N. C., Vajdos, F., Fee, L., Grimsley, G. & Gray, T. (1995) How to measure and predict the molar absorption coefficient of a protein. Prot. Sci. 4, 2411-2423]: 1 absorption unit (1 OD) at 280 nm corresponds to 1.101 mg/ml of consensus phytase-1, 1.068 mg/ml of consensus phytase-7, and 1.039 mg/ml of consensus phytase-10.

In case of pH-optimum curves, the purified enzymes were diluted in 10 mM sodium acetate, pH 5.0. Incubations were started by mixing aliquots of the diluted protein with an equal volume of 1% phytic acid (\approx 10 mM) in a series of different buffers: 0.4 M glycine/HCl, pH 2.5; 0.4 M acetate/NaOH, pH 3.0, 3.5, 4.0, 4.5, 5.0, 5.5; 0.4 M imidazole/HCl, pH 6.0, 6.5; 0.4 M Tris/HCl pH 7.0, 7.5, 8.0, 8.5, 9.0. Control experiments showed

that pH was only slightly affected by the mixing step. Incubations were performed for 15 min at 37°C as described above.

For determination of the substrate specificities of the phytases, phytic acid in the assay mixture was replaced by 5 mM concentrations of the respective phosphate compounds. Besides, the activity tests were performed as described above.

For determination of the temperature optimum, enzyme (100 µl) and substrate solution (100 µl) were pre-incubated for 5 min at the given temperature. The reaction was started by addition of the substrate solution to the enzyme. After 15 min of incubation, the reaction was stopped with trichloroacetic acid, and the amount of phosphate released was determined.

The pH-optimum of consensus phytase-1 was around pH 6.0-6.5 (70 U/mg). Introduction of the Q50T mutation shifted the pH-optimum to pH 6.0 (130 U/mg). Introduction of the K91A mutation further shifted the pH optimum into the more acidic pH-range. Comparable effects of the Q50T and K91A mutations were also observed for consensus phytase-10 and for further stabilized consensus phytase variants (Figures 14 and 15).

Consensus phytase-7, which was constructed to transfer the catalytic characteristics of *A. niger* NRRL 3135 phytase to consensus phytase-1, had a pH-profile very similar to that of *A. niger* NRRL 3135 phytase (see Figure 18). The substrate specificity also resembled more that of *A. niger* NRRL 3135 phytase than that of consensus phytase-1.

The temperature optimum of consensus phytase-1 (71°C) was 16-26°C higher than the temperature optima of the wild-type phytases (45-55°C, Table 7) that were used to calculate the consensus sequence. The improved consensus phytase-10 showed a further increase of its temperature optimum to 80°C (Figure 13).

The temperature optimum of consensus phytase-1-thermo[8] was found to be in the same range (78°C) when using the supernatant of an overproducing *S. cerevisiae* strain. The highest temperature optimum reached of 82°C was determined for 5 consensus phytase-10-thermo[3]-Q50T-K91A. Table 7

Temperature optima and Tm-values of consensus phytase and of the phytases from *A. fumigatus*, *A. niger*, *E. nidulans*, and *M. thermophila*.

10

The determination of the temperature optimum was performed as described in Example 9. The Tm-values were determined by differential scanning calorimetry as described in Example 10.

| Phytase | Optimum temperature ($^{\circ}\text{C}$) | Tm ($^{\circ}\text{C}$) |
|--|---|---------------------------|
| <i>Aspergillus niger</i> NRRL 3135 | 55 | 63.3 |
| <i>Aspergillus fumigatus</i> ATCC 13073 | 55 | 62.5 |
| <i>Aspergillus terreus</i> 9A-1 | 49 | 57.5 |
| <i>Aspergillus terreus</i> cbs116.46 | 45 | 58.5 |
| <i>Emericella nidulans</i> | 45 | 55.7 |
| <i>Myceliophthora thermophila</i> | 55 | - |
| <i>Talaromyces thermophilus</i> | 45 | - |
| Consensus phytase-10-thermo[5]-Q50T-K91A | - | 90.4 |
| Consensus-phytase-10-thermo[3]-Q50T-K91A | 82 | 89.3 |

55

| | | |
|---|----|------|
| Consensus-phytase-10-thermo [3] -Q50T | 82 | 88.6 |
| Consensus-phytase-10 | 80 | 85.4 |
| Consensus phytase-1-thermo [11] -Q50T-K91A | - | 88.0 |
| Consensus phytase-1-thermo [11] -Q50T | - | 88.5 |
| Consensus-phytase-1-thermo [8] -Q50T-K91A | - | 85.7 |
| Consensus-phytase-1-thermo [8] -Q50T | 78 | 84.7 |
| Consensus-phytase-1-thermo [8] | 81 | - |
| Consensus-phytase-1-thermo [3] | 75 | - |
| Consensus-phytase-1-Q50T | - | 78.9 |
| Consensus-phytase-1 | 71 | 78.1 |
| Aspergillus fumigatus α -mutant Q51T | 60 | 67.0 |
| Aspergillus fumigatus α -mutant, plus mutations E59A, S154N, R329H, S364T, G404A | 63 | - |
| Aspergillus fumigatus "optimized" alpha-mutant, plus mutation K92A | 63 | - |

Example 10Determination of the melting temperature by differential scanning calorimetry (DSC)

5 In order to determine the unfolding temperature of the phytases, differential scanning calorimetry was applied as described by Brugger et al., 1997 [Brugger, R., Mascarello, F., Augem, S., van Loon, A. P. G. M. & Wyss, M. (1997). Thermal denaturation of phytases and pH 2.5 acid phosphatase studied by
10 differential scanning calorimetry. In The Biochemistry of phytate and phytase (eds. Rasmussen, S.K.; Raboy, V.; Dalbøge, H. and Loewus, F.; Kluwer Academic Publishers, Dordrecht, the Netherlands]. Solutions of 50-60 mg/ml of homogeneous phytase were used for the tests. A constant heating rate of 10°C/min was applied up to 90-95°C.
15

The determined melting points confirm the results obtained for the temperature optima (Table 7). The most stable consensus phytase designed so far is consensus phytase-10-thermo[3]-Q50T-K91A showing a melting temperature under the chosen conditions
20 of 89.3°C. This is 26.0 to 33.6°C higher than the melting temperature of the wild-type phytases used.

Example 11Transfer of basidiomycete phytase active site into
25 consensus phytase-10-thermo[3]-Q50T-K91A

As described previously (Example 5), mutations derived from the basidiomycete phytase active sites were introduced into consensus phytase-10. The following five constructs a) to e) were prepared:

30 a) The construct called consensus phytase-12, and it comprises a selected number of active site residues of the

basidio consensus sequence. Its amino acid sequence is shown in Fig. 21 (the first 26 amino acids form the signal peptide; positions differing from consensus phytase-10-thermo[3]-Q50T-K91A are underlined);

5 b) a cluster of mutations (Cluster II) was transferred to the consensus phytase-1 and -10 sequences, viz.: S80Q, Y86F, S90G, K91A, S92A, K93T, A94R, Y95I;

10 c) in a similar way, another cluster of mutations (Cluster III) was transferred, viz.: T129V, E133A, Q134N, M136S, V137S, N138Q, S139A;

d) in a similar way, a further cluster of mutations (Cluster IV) was transferred, viz.: A168D, E171T, K172N, F173W;

e) and finally, a further cluster of mutations (Cluster V) was transferred, viz.: Q297G, S298D, G300D, Y305T.

15 These constructs were expressed as described in Examples 6 to 8.

Example 12

Phytase alignment using GAP

20 The phytases described herein - i.e. the amino acid sequences as well as the corresponding DNA sequences - were aligned against each other. Also some other phytases were correspondingly aligned, viz. the following:

- the consensus phytase-1 described in EP 897985;
- 25 - the phytase derived from Aspergillus niger (ficum) NRRL 3135 (A. niger NRRL3135) described in EP 420358;
- the phytases derived from Aspergillus fumigatus ATCC 13073 (A. fumigatus 13073); Aspergillus fumigatus ATCC 32239 (A. fumigatus 32239); Aspergillus terreus cbs116.46 (A.terreus cbs);
- 30 Emericella nidulans (E. nidulans); and Talaromyces thermophilus (T. thermophilus) - all described in EP 897010;

- the phytases derived from *Myceliophthora thermophila* (*M. thermophila*) ; and *Aspergillus terreus* 9-A1 (*A. terreus* 9-A1) - both described in EP 684313;
- the phytase derived from *Thermomyces lanuginosus* (*T. lanuginosus*) described in WO 9735017 (PCT/US97/04559) ;
- the phytases derived from *Agrocybe pediades* (*A. pediades*) , *Paxillus involutus* 1 and 2 (*P. involutus* phyA1 and phyA2); and *Trametes pubescens* (*T. pubescens*) - all described in WO 98/28409; and
- the phytase derived from *Peniophora lycii* (*P. lycii*) described in WO 98/28408.

For the alignments, the program GAP was used with the settings as described above.

For polypeptide comparisons, the signal peptides were included with the exception of comparisons with consensus phytase-11.

The results of the amino acid sequence comparisons are shown in Table 8 below. The first number in each cell is the amino acid similarity, the second number is the amino acid identity.

For DNA sequence comparisons, the signal sequence was always included. The results are shown in Table 9 below.

This invention comprises e.g. the following embodiments (A) to (J) that are described below.

In these embodiments, when determining % identity or % similarity at the amino acid level for another phytase, its amino acid sequence is aligned with the reference sequence (e.g. in embodiment (A) the consensus phytase-10 amino acid sequence), using an alignment program such as GAP referred to above. Percentage identity, as well as percentage similarity, is

calculated by the program. The amino acid sequence of the other phytase may or may not include the signal peptide.

When determining % identity on the DNA level for another phytase-encoding DNA, this DNA sequence is aligned with the 5 reference sequence [e.g. in embodiment (A) nucleotides 12-1412 of SEQ ID NO: 25 (the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5], using an alignment program such as GAP referred to above. Percentage identity is calculated by the program. The DNA sequence encoding the other phytase can be a 10 genomic DNA sequence including introns, or it can be a cDNA sequence. It may or may not include the signal peptide-encoding part.

When determining hybridization, the probe to be used is the specified DNA sequence [e.g. in embodiment (A) nucleotides 15 12-1412 of SEQ ID NO: 25 (the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5)]. The DNA sequence encoding the other phytase can be a genomic DNA sample which contains a phytase-encoding DNA-sequence; a purified genomic DNA sequence (purified with respect to the phytase-encoding DNA sequence); or 20 it can be a phytase-encoding cDNA sequence, preferably purified or amplified, e.g. PCR-amplified. The phytase-encoding DNA, whatever type, may or may not include the signal peptide-encoding part. Suitable hybridization conditions are referred to above.

25 The term "DNA sequence" includes such fragments or parts of the herein exemplified DNA sequences, as long as they are capable of encoding an active enzyme (e.g. phytase).

The term "amino acid sequence" includes such fragments or parts of the herein exemplified amino acid sequences, as long 30 as they are enzymatically active (e.g. displaying phytase activity).

(A) Phytases and corresponding DNA sequences related to consensus phytase-10 (CP10, Fcp 10)

A phytase that comprises an amino acid sequence which is at least 93.80%; or at least 94, 94.5, 95, 95.5, 96, 96.5, 97, 5 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10 (Fcp10) as shown in Fig. 5.

A phytase that comprises an amino acid sequence which is at least 95.09%; or at least 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of 10 consensus phytase-10.

A phytase which is encoded by a DNA sequence which is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5.

15 A DNA sequence which encodes a phytase and which (i) is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 20 (Fcp10) as shown in Fig. 5. A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP10, CP10-thermo[3]-Q50T, K91A, CP1-thermo[8], CP1-thermo[8]Q50T, K91A.

A DNA sequence which encodes a phytase comprising an amino 25 acid sequence which is at least 93.80%; or at least 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10 (Fcp10) as shown in Fig. 5.

(B) Phytases and corresponding DNA sequences related to consensus phytase-10-thermo[3]-Q50T-K91A

A phytase which comprises an amino acid sequence which is at least 93.37%; or at least 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 5 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A phytase which comprises an amino acid sequence which is at least 94.66%; or at least 95.0, 95.5, 96, 96.5, 97, 97.5, 98, 10 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A phytase which is encoded by a DNA sequence which is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 12-1412 of the DNA sequence of 15 consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A DNA sequence which encodes a phytase and which (i) is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to 20 nucleotides 12-1412 of the DNA sequence of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8. A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP10, CP10-thermo[3]-Q50T-K91A, CP1-thermo[8], or CP1-thermo[8]-Q50T-K91A.

25 A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 93.37%; or at least 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

(C) Phytases and corresponding DNA sequences related to consensus phytase-1-thermo[8]

A phytase which comprises an amino acid sequence which is at least 98.30%; or at least 98.5, 99, 99.5% identical to the 5 sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

A phytase which comprises an amino acid sequence which is at least 98.51%; or at least 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown 10 in Fig. 7; backmutations T50Q and A91K to be added).

A phytase which is encoded by a DNA sequence which is at least 98.73%; or at least 99, 99.5% identical to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

15 A DNA sequence which encodes a phytase and which (i) is at least 98.73%; or at least 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8] (as shown in Fig. 7; 20 backmutations T50Q and A91K to be added). A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP1-thermo[8], CP1-thermo[8]-Q50T-K91A.

A DNA sequence which encodes a phytase comprising an amino 25 acid sequence which is at least 98.30%; or at least 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

(D) Phytases and corresponding DNA sequences related to consensus phytase-1-thermo[8]-Q50T-K91A

A phytase which comprises an amino acid sequence which is at least 97.87%; or at least 98, 98.5, 99, 99.5% identical to 5 the sequence of amino acids 1-467 of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7.

A phytase which comprises an amino acid sequence which is at least 98.08%; or at least 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8]-10 Q50T-K91A as shown in Fig. 7.

A phytase which is encoded by a DNA sequence which is at least 98.37%; or at least 98.5, 99, 99.5% identical to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7.

15 A DNA sequence which encodes a phytase and which (i) is at least 98.37%; or at least 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7. A 20 suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP1-thermo[8], CP1-thermo[8]-Q50T-K91A.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 97.87%; or at least 98, 98.5, 25 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase 1-thermo[8]-Q50T-K91A as shown in Fig. 7.

(E) Phytases and corresponding DNA sequences related to consensus phytase-11

30 A phytase that comprises an amino acid sequence which is at least 90.71%; or at least 91, 91.5, 92, 92.5, 93, 93.5, 94,

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94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

A phytase that comprises an amino acid sequence which is at least 92.07%; or at least 92.5, 93, 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

A DNA sequence that encodes a phytase comprising an amino acid sequence which is at least 90.71%; or at least 91, 91.5, 92, 92.5, 93, 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

(F) Phytases and corresponding DNA sequences related to A. fumigatus alpha-mutant

A phytase that comprises an amino acid sequence which is at least 97.17%; or at least 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of A. fumigatus alpha-mutant (phytase) as shown in Fig. 9.

A phytase that comprises an amino acid sequence that is at least 97.82%; or at least 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of A. fumigatus alpha-mutant (phytase) as shown in Fig. 9.

A phytase which is encoded by a DNA sequence which is at least 96.13%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 1-1401 of the DNA sequence of A. fumigatus ATCC 13073 alpha-mutant (phytase) as shown in Fig. 9.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 97.17%; or at least 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467

of A. fumigatus ATCC 13073 alpha-mutant (phytase) as shown in Fig. 9.

A DNA sequence which encodes a phytase and which (i) is at least 96.13%; or 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; 5 or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1401 of the DNA sequence of A. fumigatus ATCC 13073 alpha-mutant (phytase) shown in Fig. 9. A suitable negative control is DNA encoding A. fumigatus 13073 phytase. A suitable positive control is DNA 10 encoding any one of the A. fumigatus ATCC 13073 alpha mutant phytase or the optimised alpha-mutant.

(G) Phytases and corresponding DNA sequences related to the optimized A. fumigatus alpha-mutant

15 A phytase that comprises an amino acid sequence that is at least 96.08%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of the phytase of the optimized A. fumigatus alpha-mutant.

20 A phytase that comprises an amino acid sequence that is at least 96.74%; or at least 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of the phytase of the optimized A. fumigatus alpha-mutant.

25 A phytase which is encoded by a DNA sequence which is at least 95.63%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 1-1401 of the DNA sequence encoding the optimized A. fumigatus alpha-mutant phytase.

30 A DNA sequence that encodes a phytase comprising an amino acid sequence that is at least 96.08%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the optimized A. fumigatus alpha-mutant phytase.

A DNA sequence which encodes a phytase and which (i) is at least 95.63%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, very high stringency conditions to 5 nucleotides 1-1401 of the DNA sequence encoding the optimized *A. fumigatus* alpha-mutant phytase.

A suitable negative control is DNA encoding *A. fumigatus* ATCC 13073 phytase. A suitable positive control is DNA encoding any one of the *A. fumigatus* ATCC 13073 alpha mutant phytase of 10 the optimised alpha-mutant.

(H) Phytases and corresponding DNA sequences related to consensus phytase-7

A phytase that comprises an amino acid sequence which is 15 at least 94.87%; or at least 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-7 as shown in Fig. 10.

A phytase that comprises an amino acid sequence which is at least 95.30%; or at least 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 20 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-7 as shown in Fig. 10.

A phytase which is encoded by a DNA sequence which is at least 96.38%; or 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase-25 7 shown in Fig. 10.

A DNA sequence which encodes a phytase and which (i) is at least 96.38%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 12-1412 30 of the DNA sequence of consensus phytase-7 as shown in Fig. 10.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 94.87%; or at least 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-7 as shown in
5 Fig. 10.

(I) Phytases related to basidio consensus phytase

A phytase which comprises an amino acid sequence which is at least 76.23%; or at least 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 94.5, 95, 95.5, 96, 96.5, 10 97, 97.5, 98, 98.5, 99, 99.5% identical to the combined sequence of (i) amino acids 1-441 of basidio consensus phytase shown in Fig. 3, and (ii) amino acids 1-26 shown in Fig. 5 (the sequence of (ii) to be added at the N-terminus of the sequence of (i)).

A phytase that comprises an amino acid sequence which is 15 at least 79.50%; or at least 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-441 of basidio consensus phytase as shown in Fig. 3.

(J) Phytases related to consensus phytase-12

20 A phytase which comprises an amino acid sequence which is at least 70, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-12 as shown in Fig. 21.

25 A phytase which comprises an amino acid sequence which is at least 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-12 as shown in Fig. 21.

Table 8

Comparison of phytase amino acid sequences

| Phytase | CP10 | CP10-thermo [3] - Q50T-K91A | CP1-thermo [8] - Q50T-K91A | CP11 | CP7 | Basidio | A. fumigatus alpha-mutant | A. fumigatus alpha-mutant (opt.) |
|----------------------------|-------------|-----------------------------|----------------------------|-------------|-------------|-------------|---------------------------|----------------------------------|
| Consensus phytase-1 | 95.08/93.79 | 94.65/93.36 | 98.50/98.29 | 98.07/97.86 | 92.06/90.70 | 95.29/94.86 | 69.42/62.16 | 85.59/82.58 |
| <i>A. niger</i> NRRL3135 | 79.48/76.46 | 79.05/76.03 | 80.35/77.75 | 79.91/77.32 | 79.27/76.31 | 84.02/81.64 | 67.19/59.32 | 74.07/70.11 |
| <i>A. terreus</i> 9-A1 | 76.04/72.11 | 75.82/71.90 | 76.47/72.33 | 76.25/72.11 | 76.51/73.02 | 75.76/71.18 | 65.39/58.02 | 69.67/64.84 |
| <i>A. terreus</i> CBS | 79.04/75.11 | 78.82/74.89 | 79.48/75.76 | 79.26/75.55 | 77.19/73.27 | 79.17/75.00 | 66.92/59.65 | 72.59/67.76 |
| <i>E. nidulans</i> | 78.70/74.35 | 78.26/73.91 | 79.78/75.87 | 79.35/75.44 | 80.56/76.62 | 76.96/73.04 | 67.20/58.13 | 72.39/67.83 |
| <i>A. fumigatus</i> 13073 | 82.93/80.31 | 82.50/79.87 | 82.31/79.04 | 81.88/78.60 | 81.36/78.64 | 80.13/76.20 | 63.54/57.91 | 97.82/97.16 |
| <i>A. fumigatus</i> 322239 | 81.30/77.39 | 80.87/76.96 | 81.09/77.61 | 80.65/77.17 | 79.95/76.08 | 79.13/75.22 | 63.61/54.97 | 90.22/86.52 |
| <i>T. thermophilus</i> | 77.83/73.84 | 77.38/73.39 | 78.67/74.89 | 78.22/74.44 | 78.47/74.76 | 76.51/73.15 | 61.54/54.36 | 72.01/66.82 |
| <i>M. thermophilia</i> | 69.16/62.81 | 69.48/63.33 | 69.27/62.84 | 69.59/63.36 | 69.65/63.06 | 68.82/62.13 | 65.56/57.91 | 66.21/58.45 |
| <i>T. lanuginosus</i> | 73.52/66.70 | 73.06/66.44 | 71.92/64.61 | 71.46/64.16 | 74.21/68.86 | 69.50/62.62 | 67.20/57.41 | 68.91/61.02 |
| <i>P. lycii</i> | 64.92/59.10 | 64.91/59.37 | 64.46/58.09 | 64.46/58.36 | 65.03/59.84 | 63.13/56.50 | 77.75/73.07 | 64.08/57.11 |
| <i>A. pediades</i> | 64.51/51.81 | 64.86/51.94 | 62.98/51.41 | 63.33/51.54 | 64.50/52.30 | 63.05/51.15 | 78.92/74.71 | 61.64/52.38 |
| <i>P. involutus</i> 1 | 66.67/58.07 | 66.67/58.33 | 64.84/56.51 | 64.84/56.77 | 63.30/54.52 | 65.33/56.53 | 79.49/76.22 | 59.59/51.81 |
| <i>P. involutus</i> 2 | 65.54/55.70 | 65.30/55.53 | 66.85/56.87 | 66.58/56.68 | 66.30/56.35 | 64.27/54.13 | 78.09/74.59 | 61.26/52.62 |

| | | | | | | | | | |
|-------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| T. pubescens | 65.46/57.22 | 65.72/57.47 | 62.89/55.67 | 63.14/55.93 | 65.03/57.65 | 63.28/56.51 | 78.34/75.12 | 64.08/57.11 | 62.30/55.24 |
| CP10 | - | 99.57/99.57 | 96.57/95.50 | 96.15/95.08 | 95.02/94.56 | 91.01/89.29 | 70.22/62.28 | 85.13/82.76 | 85.99/83.62 |
| CP10t [3]Q50TK91A | 99.57/99.57 | - | 96.15/95.08 | 96.57/95.50 | 94.56/94.10 | 90.58/88.87 | 70.47/62.28 | 85.13/82.76 | 85.99/83.62 |
| CP1thermo [8] | 96.57/95.50 | 96.15/95.08 | - | 99.57/99.57 | 93.42/92.29 | 94.43/93.79 | 68.40/60.74 | 84.52/81.94 | 85.38/82.80 |
| CP1t [8]Q50TK91A | 96.15/95.08 | 96.57/95.50 | 99.57/99.57 | - | 92.97/91.84 | 94.00/93.36 | 68.64/60.74 | 84.52/81.94 | 85.38/82.80 |
| CP11 | 95.02/94.56 | 94.56/94.10 | 93.42/92.29 | 92.97/91.84 | - | 88.44/86.62 | 68.27/59.73 | 82.23/79.73 | 83.37/80.87 |
| CP7 | 91.01/89.29 | 90.58/88.87 | 94.43/93.79 | 94.00/93.36 | 88.44/86.62 | - | 69.80/62.69 | 81.94/78.71 | 81.72/78.50 |
| Basidio | 70.22/62.28 | 70.47/62.28 | 68.40/60.74 | 68.64/60.74 | 68.27/59.73 | 69.80/62.69 | - | 65.97/60.52 | 66.41/60.68 |
| A. fumigatus alpha-mut. | 85.13/82.76 | 85.13/82.76 | 84.52/81.94 | 84.52/81.94 | 82.23/79.73 | 81.94/78.71 | 65.97/60.52 | - | 98.93/98.93 |
| A. fum alpha-mut opt. | 85.99/83.62 | 85.99/83.62 | 85.38/82.80 | 85.38/82.80 | 83.37/80.87 | 81.72/78.50 | 66.41/60.68 | 98.93/98.93 | - |

Table 9

Comparison of phytase encoding DNA sequences

| Phytase | CP10 | CP10-thermo [3]-Q50T-K91A | CP1-thermo [8]-Q50T-K91A | CP7 | Basidio | A. fumigatus alpha-mutant (opt.) |
|---------------------------|-------|---------------------------|--------------------------|-------|---------|----------------------------------|
| Consensus phytase-1 | 95.87 | 95.87 | 98.72 | 98.36 | 96.37 | 65.46 |
| <i>A. niger</i> NRRL3135 | 65.10 | 64.82 | 66.10 | 65.74 | 67.52 | 50.68 |
| <i>A. terreus</i> 9-A1 | 61.74 | 61.53 | 62.17 | 62.03 | 60.53 | 49.40 |
| <i>A. terreus</i> cbs | 62.52 | 62.30 | 63.02 | 62.88 | 61.45 | 49.74 |
| <i>E. nidulans</i> | 65.08 | 64.94 | 65.30 | 65.01 | 64.22 | 49.92 |
| <i>A. fumigatus</i> 13073 | 65.66 | 65.38 | 64.19 | 64.08 | 63.65 | 48.27 |
| <i>T. thermophilus</i> | 62.52 | 62.50 | 62.53 | 62.66 | 62.00 | 52.19 |
| <i>M. thermophila</i> | 55.51 | 55.15 | 55.36 | 55.22 | 53.91 | 48.44 |
| <i>T. lanuginosus</i> | 57.56 | 57.20 | 56.76 | 56.47 | 62.00 | 44.66 |
| <i>P. lycii</i> | 45.76 | 46.51 | 45.14 | 55.21 | 55.46 | 58.50 |
| <i>A. pediades</i> | 49.89 | 49.89 | 49.89 | 50.11 | 45.54 | 61.66 |
| <i>P. involutus</i> 1 | 48.32 | 49.03 | 47.81 | 47.96 | 49.59 | 59.80 |
| <i>P. involutus</i> 2 | 48.24 | 49.00 | 48.08 | 48.63 | 47.94 | 60.16 |
| <i>T. phibescens</i> | 47.00 | 47.17 | 46.46 | 47.62 | 46.83 | 60.37 |
| CP10 | - | 99.43 | 96.40 | 96.05 | 93.73 | 66.40 |

71

| | | | | | | | | |
|-------------------------|-------|-------|-------|-------|-------|-------|-------|-------|
| CPI0t [3]Q50TK91A | 99.43 | - | 96.37 | 96.58 | 93.45 | 66.29 | 67.81 | 68.24 |
| Cp1thermo [8] | 96.40 | 96.37 | - | 99.65 | 95.30 | 65.40 | 66.74 | 67.17 |
| CPIlt [8]Q50TK91A | 96.05 | 96.58 | 99.65 | - | 94.94 | 65.47 | 66.74 | 67.17 |
| CP7 | 93.73 | 93.45 | 95.30 | 94.94 | - | 64.56 | 65.88 | 65.88 |
| Bastidio | 66.40 | 66.29 | 65.40 | 65.47 | 64.56 | - | 50.41 | 50.49 |
| A.fumigatus alpha-mut. | 67.81 | 67.81 | 66.74 | 66.74 | 65.88 | 50.41 | - | 99.50 |
| A. fum alpha-mut - opt. | 68.24 | 68.24 | 67.17 | 67.17 | 65.88 | 50.49 | 99.50 | - |

What is claimed is:

1. A phytase that comprises an amino acid sequence which is at least 93.80% identical to the sequence of amino acids 1-467 of 5 consensus phytase-10 (SEQ ID NO: 26).

2. A phytase that is encoded by a DNA sequence that is at least 95.88% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 (SEQ ID NO: 25).

10

3. A phytase that comprises
an amino acid sequence chosen from

(i) SEQ ID NO: 26, or amino acids 1-438 thereof; or
an amino acid sequence encoded by

15 (ii) nucleotides 12-1412, or 90-1412 of SEQ ID NO: 25.

4. A phytase that comprises
an amino acid sequence chosen from

(i) consensus phytase-10-thermo[3],
20 (ii) variants of (i), further including the mutations Q50T, K91A, or (Q50T+K91A), the latter variant being shown in Fig. 8,

(iii) amino acids 27-467 of any of the sequences of (i)
and (ii),

25 (iv) SEQ ID NO: 31, or amino acids 1-441 thereof; or
an amino acid sequence encoded by

(v) nucleotides 1-1401, or 79-1401 of SEQ ID NO: 30.

5. A phytase that comprises

30 an amino acid sequence chosen from

(i) consensus phytase-1-thermo[8],

(ii) variants of (i), further including the mutations Q50T, K91A, or (Q50T+K91A), the latter variant being shown in Fig. 7,

5 (iii) amino acids 27-467 of any of the sequences of (i) and (ii), or

(iv) SEQ ID NO: 29, or amino acids 1-441 thereof; or an amino acid sequence encoded by

(v) nucleotides 1-1407, or 79-1407 of SEQ ID NO: 28.

10 6. A phytase that comprises the amino acid sequence of consensus phytase-11 (SEQ ID NO: 27).

7. A DNA sequence that comprises a DNA-sequence encoding a phytase of claim 1.

15

8. A DNA sequence that comprises a DNA-sequence encoding a phytase, wherein the phytase-encoding DNA-sequence is (i) at least 95.88% identical, or (ii) hybridizes under high stringency conditions, to nucleotides 12-1412 of the DNA sequence of 20 consensus phytase-10 (SEQ ID NO: 25).

9. A DNA sequence that comprises a DNA-sequence that encodes a phytase, wherein the phytase comprises an amino acid sequence that is at least 93.80% identical to the sequence of amino acids 25 1-467 of consensus phytase 10 (SEQ ID NO: 26).

10. A DNA sequence that comprises a DNA-sequence that encodes a phytase, and wherein the phytase-encoding DNA-sequence comprises

30 (i) nucleotides 12-1412, or 90-1412 of the DNA sequence of consensus phytase-10 (SEQ ID NO: 25);

- (ii) nucleotides 1-1401, or 79-1401 of the DNA sequence of consensus phytase-10-thermo[3]-Q50T-K91A (SEQ ID NO: 30); or
5 (iii) nucleotides 1-1401, or 79-1401 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A (SEQ ID NO: 28).

11. A vector comprising a DNA sequence according to claim 7.

10 12. A microbial host cell comprising a DNA sequence according to claim 7, or the vector according to claim 11.

13. A process for producing a phytase, the process comprising culturing the host cell according to claim 12 under conditions permitting the production of the phytase, and recovering the phytase from the culture broth.
15

14. A food, feed or pharmaceutical composition comprising a phytase of claim 1.

ABSTRACT

This invention relates to improved phytases, preferably phytases of an increased thermostability, and a process of producing them. In particular, stabilizing amino acid mutations 5 are introduced into a homologous protein, or the active site of a phytase is replaced in part or in toto. The corresponding DNA sequences and methods of preparing them are also disclosed, as are methods of producing the improved phytases, and the use thereof. Specific variants of *Aspergillus fumigatus* phytase and 10 of consensus phytases are disclosed.

DOCUMENT EVIDENCE

| | | | |
|-----------------------|------------|--|-----|
| | | 1 | 50 |
| A. terreus 9A-1 | KhsDCNSVDh | GYQCFPELSh kWGLYAPYFS LQDESPFP1D VPEDChITFV | |
| A. terreus cbs | NhsDCTSVDr | GYQCFPELSh kWGLYAPYFS LQDESPFP1D VPDDChITFV | |
| A. niger var. awamori | NqSTCDTVDQ | GYQCFSETSH LWGQYAPFFS LANESAISPD VPAGCrVTFA | |
| A. niger T213 | NqSSCDTVDQ | GYQCFSETSH LWGQYAPFFS LANESVISPD VPAGCrVTFA | |
| A. niger NRRL3135 | NqSSCDTVDQ | GYQCFSETSH LWGQYAPFFS LANESVISPE VPAGCrVTFA | |
| A. fumigatus 13073 | GSKSCDTVD1 | GYQCSPATSH LWGQYSPFFS LEDELSVSSK LPKDCCrITLV | |
| A. fumigatus 32722 | GSKSCDTVD1 | GYQCSPATSH LWGQYSPFFS LEDELSVSSK LPKDCCrITLV | |
| A. fumigatus 58128 | GSKSCDTVD1 | GYQCSPATSH LWGQYSPFFS LEDELSVSSK LPKDCCrITLV | |
| A. fumigatus 26906 | GSKSCDTVD1 | GYQCSPATSH LWGQYSPFFS LEDELSVSSK LPKDCCrITLV | |
| A. fumigatus 32239 | GSKACDTVE1 | GYQCSPGTSH LWGQYSPFFS LEDELSVSSD LPKDCCrVTFA | |
| E. nidulans | QNHSCNTADG | GYQCFPNVSH VWGQYSPYFS IEQESAISeD VPHGCeVTFV | |
| T. thermophilus | DHSCTNTEG | GYQCPEISH SWGQYSPFFS LADQSEISPD VPQNCKITFV | |
| M. thermophila | ESRPCDTPd1 | GFQCgTAISH FWGQYSPYFS VpSELDaS.. IPDDCeVTFA | |
| Consensus | NSHSCDTVDG | GYQCFPEISH LWGQYSPYFS LEDESAISPD VPDDC-VTFV | |
| Consensus phytase | NSHSCDTVDG | GYQCFPEISH LWGQYSPYFS LEDESAISPD VPDDCRVTFA | |
| | | 51 | 100 |
| A. terreus 9A-1 | QVLARHGARS | PThSKtKAYA AtIAAIQKSA TaFpGKYAFL QSYNYSLDSE | |
| A. terreus cbs | QVLARHGARS | PTDSKtKAYA AtIAAIQKNA TaLpGKYAFL KSYNYSMGSE | |
| A. niger var. awamori | QVLSRHGARY | PTESKgKkYS ALIEEIQQNV TtFDGKYAFL KTNYSLGAD | |
| A. niger T213 | QVLSRHGARY | PTESKgKkYS ALIEEIQQNV TtFDGKYAFL KTNYSLGAD | |
| A. niger NRRL3135 | QVLSRHGARY | PTDSKgKkYS ALIEEIQQNA TtFDGKYAFL KTNYSLGAD | |
| A. fumigatus 13073 | QVLSRHGARY | PTSSKsKkYK KLVTAIQaNA TdFKGKFAFL KTNYTLGAD | |
| A. fumigatus 32722 | QVLSRHGARY | PTSSKsKkYK KLVTAIQaNA TdFKGKFAFL KTNYTLGAD | |
| A. fumigatus 58128 | QVLSRHGARY | PTSSKsKkYK KLVTAIQaNA TdFKGKFAFL KTNYTLGAD | |
| A. fumigatus 26906 | QVLSRHGARY | PTSSKsKkYK KLVTAIQaNA TdFKGKFAFL KTNYTLGAD | |
| A. fumigatus 32239 | QVLSRHGARY | PTASKsKkYK KLVTAIQKNA TeFKGKFAFL ETNYTLGAD | |
| E. nidulans | QVLSRHGARY | PTESKsKAYS GLIEAIQKNA TsFwGQYAFL ESYNYTLGAD | |
| T. thermophilus | QLLSRHGARY | PTSSKtElys QLISRIQKTA TayKGyYAFL KDYrYqLGAN | |
| M. thermophila | QVLSRHGARA | PT1KRaaSYv DLIDrIHhGA IsYgPgYEFL RTYDYTLGAD | |
| Consensus | QVLSRHGARY | PTSSK-KAYS ALIEAIQKNA T-FKGKYAFL KTNYTLGAD | |
| Consensus phytase | QVLSRHGARY | PTSSKSKAYS ALIEAIQKNA TAFKGKYAFL KTNYTLGAD | |
| | | 101 | 150 |
| A. terreus 9A-1 | ELTPFGrNQL | rD1GaQFYeR YNALTRhInP FVRATDASRV hESAekFVEG | |
| A. terreus cbs | NLTPFGrNQL | qD1GaQFYRR YDTLTrhInP FVRAADSSRV hESAekFVEG | |
| A. niger var. awamori | DLTPFGEQEL | VNSGIKFYQR YESLTRNIIP FIRSSGSSRV IASGEKFIEG | |
| A. niger T213 | DLTPFGEQEL | VNSGIKFYQR YESLTRNIIP FIRSSGSSRV IASGEKFIEG | |
| A. niger NRRL3135 | DLTPFGEQEL | VNSGIKFYQR YESLTRNIVP FIRSSGSSRV IASGKKFIEG | |
| A. fumigatus 13073 | DLTPFGEQQL | VNSGIKFYQR YKALARSVVP FIRASGSDRV IASGEKFIEG | |
| A. fumigatus 32722 | DLTPFGEQQL | VNSGIKFYQR YKALARSVVP FIRASGSDRV IASGEKFIEG | |
| A. fumigatus 58128 | DLTPFGEQQL | VNSGIKFYQR YKALARSVVP FIRASGSDRV IASGEKFIEG | |
| A. fumigatus 26906 | DLTAFGEQQL | VNSGIKFYQR YKALARSVVP FIRASGSDRV IASGEKFIEG | |
| A. fumigatus 32239 | DLTPFGEQQM | VNSGIKFYQR YKALAgSVVP FIRSSGSDRV IASGEKFIEG | |
| E. nidulans | DLT1FGENQM | VDSGaKFYRR YKNLARKnTP FIRASGSDRV VASAekFING | |
| T. thermophilus | DLTPFGENQM | IQ1GIKFYnH YKSLARNaVP FVRCSGSDRV IASGr1FIEG | |
| M. thermophila | ELTRtGQQQM | VNSGIKFYRR YRALARKsIP FVRTAGqDRV VhSAENFTQG | |
| Consensus | DLTPFGENQM | VNSGIKFYRR YKALARK-VP FIRASGSDRV IASAekFIEG | |
| Consensus phytase | DLTPFGENQM | VNSGIKFYRR YKALARKIVP FIRASGSDRV IASAekFIEG | |

| | | |
|-----------------------|---|-----|
| | 151 | 200 |
| A. terreus 9A-1 | FQTAQDDHh ANpHQPSPrV DVaIPEGSAY NNTLEHS1CT AFES...STV | |
| A. terreus cbs | FQNARqGDPh ANpHQPSPrV DVVIPEGTAY NNTLEHSICT AFEA...STV | |
| A. niger var. awamori | FQSTKLkDPr AcpqQSSPKI DVVISEASSs NNTLDPGTCT VFED...SEL | |
| A. niger T213 | FQSTKLkDPr AcpqQSSPKI DVVISEASSs NNTLDPGTCT VFED...SEL | |
| A. niger NRRL3135 | FQSTKLkDPr AcpqQSSPKI DVVISEASSs NNTLDPGTCT VFED...SEL | |
| A. fumigatus 13073 | FQqAKLADPG A.TNRAAPAI SVIIPESETF NNTLDHGVCT kFEA...SQL | |
| A. fumigatus 32722 | FQqAKLADPG A.TNRAAPAI SVIIPESETF NNTLDHGVCT kFEA...SQL | |
| A. fumigatus 58128 | FQqAKLADPG A.TNRAAPAI SVIIPESETF NNTLDHGVCT kFEA...SQL | |
| A. fumigatus 26906 | FQqAKLADPG A.TNRAAPAI SVIIPESETF NNTLDHGVCT kFEA...SQL | |
| A. fumigatus 32239 | FQqANVADPG A.TNRAAPVI SVIIPESETY NNTLDHSVCT NFEA...SEL | |
| E. nidulans | FRKAQLhDHG S..gQATPVV NVIIPEiDGF NNTLDHSTCV SFEN...DER | |
| T. thermophilus | FQSAKV1DPh SDKHDAPPtI NVIIeEGPSY NNTLDtGSCP VFED...SSg | |
| M. thermophila | FHSALLADRG STvRPT1Pyd mVVIPETAGa NNTLHND1CT AFEEgpySTI | |
| Consensus | FQSAKLADPG S-PHQASPVI NVIIPEGSGY NNTLDHGTCT AFED---SEL | |
| Consensus phytase | FQSAKLADPG SQPHQASPVI DVIIPEGSGY NNTLDHGTCT AFED...SEL | |
| | 201 | 250 |
| A. terreus 9A-1 | GDDAvANFTA VFAPAIaQRL EADLPGVqLS TDDVVnLMAM CPFETVS1TD | |
| A. terreus cbs | GDAAADNFTA VFAPAIakRL EADLPGVqLS ADDVVnLMAM CPFETVS1TD | |
| A. niger var. awamori | ADTVEANFTA TFAPSIRQRL ENDLGSVTLT DTEVTyLMDM CSFDTISTST | |
| A. niger T213 | ADTVEANFTA TFAPSIRQRL ENDLGSVTLT DTEVTyLMDM CSFDTISTST | |
| A. niger NRRL3135 | ADTVEANFTA TFVPSIRQRL ENDLGSVTLT DTEVTyLMDM CSFDTISTST | |
| A. fumigatus 13073 | GDEVAANFTA 1FAPDIRARA EkHLPGVTLT DEDVVsLMDM CSFDTVARTS | |
| A. fumigatus 32722 | GDEVAANFTA 1FAPDIRARA EkHLPGVTLT DEDVVsLMDM CSFDTVARTS | |
| A. fumigatus 58128 | GDEVAANFTA 1FAPDIRARA EkHLPGVTLT DEDVVsLMDM CSFDTVARTS | |
| A. fumigatus 26906 | GDEVAANFTA 1FAPDIRARA KkHLPGVTLT DEDVVsLMDM CSFDTVARTS | |
| A. fumigatus 32239 | GDEVEANFTA 1FAPPAIRARI EkHLPGVqLT DDDVVsLMDM CSFDTVARTA | |
| E. nidulans | ADEIEANFTA IMGPIRKRL ENDLPGIKLT NENVIyLMDM CSFDTMARTA | |
| T. thermophilus | GHDAQEKFak qFAPAIKEKI KDHLPGVDLA vSDVpyLMDL CPFETLARNh | |
| M. thermophila | GDDAQDTY1S TFAGPITARV NANLPGANLT DADTVaLMDL CPFETVASSS | |
| Consensus | GDDAEANFTA TFAPPAIRARL EADLPGVTLT DEDVV-LMDM CPFETVARTS | |
| Consensus phytase | GDDVEANFTA LFAPPAIRARL EADLPGVTLT DEDVVYLMDM CPFETVARTS | |
| | 251 | 300 |
| A. terreus 9A-1 | DAhTLSPFC DLFTATEWtq YNYL1SLDKY YGYGGGNPLG | |
| A. terreus cbs | DAhTLSPFC DLFTaaEWtq YNYL1SLDKY YGYGGGNPLG | |
| A. niger var. awamori | vDTKLSRFC DLFThdEWih YDYLQSLkKY YGHGAGNPLG | |
| A. niger T213 | vDTKLSRFC DLFThdEWih YDYLQSLkKY YGHGAGNPLG | |
| A. niger NRRL3135 | vDTKLSRFC DLFThdEWin YDYLQSLkKY YGHGAGNPLG | |
| A. fumigatus 13073 | DASQLSPFC QLFThnEWkk YNYLQSLGKY YGYGAGNPLG | |
| A. fumigatus 32722 | DASQLSPFC QLFThnEWkk YNYLQSLGKY YGYGAGNPLG | |
| A. fumigatus 58128 | DASQLSPFC QLFThnEWkk YNYLQSLGKY YGYGAGNPLG | |
| A. fumigatus 26906 | DASQLSPFC QLFThnEWkk YNYLQSLGKY YGYGAGNPLG | |
| A. fumigatus 32239 | DASELSPFC AIFThnEWkk YDYLQSLGKY YGYGAGNPLG | |
| E. nidulans | HGTELSPFC AIFTEkEWlq YDYLQSLSKY YGYGAGSPLG | |
| T. thermophilus | TDT.LSPFC AlstQeEWqa YDYYQSLGKY YGnGGGNPLG | |
| M. thermophila | sdpatadag gNGrpLSPFC rLFSEsEWra YDYLQSVGKW YGYGPGNPLG | |
| Consensus | ----- -DATELSPFC ALFTE-EW-- YDYLQSLGKY YGYGAGNPLG | |
| Consensus phytase |DATELSPFC ALFTHDEWRQ YDYLQSLGKY YGYGAGNPLG | |

Fig. 1b

| | | |
|-----------------------|---|-----|
| | 301 | 350 |
| A. terreus 9A-1 | PVQGVGWA ^N E LMARLTRAPV HDHTCVNN ^T L DASPATFPLN ATLYADFSHD | |
| A. terreus cbs | PVQGVGWA ^N E LIARLTRSPV HDHTCVNN ^T L DANPATFPLN ATLYADFSHD | |
| A. niger var. awamori | PTQGVGYa ^N E LIARLTHSPV HDDTSSNHTL DSNPATFPLN STLYADFSHD | |
| A. niger T213 | PTQGVGYa ^N E LIARLTHSPV HDDTSSNHTL DSNPATFPLN STLYADFSHD | |
| A. niger NRRL3135 | PTQGVGYa ^N E LIARLTHSPV HDDTSSNHTL DSSPATFPLN STLYADFSHD | |
| A. fumigatus 13073 | PAQGIGFTNE LIARLTRSPV QDHTSTN ^S TL vSNPATFPLN ATMYVDFSHD | |
| A. fumigatus 32722 | PAQGIGFTNE LIARLTRSPV QDHTSTN ^S TL vSNPATFPLN ATMYVDFSHD | |
| A. fumigatus 58128 | PAQGIGFTNE LIARLTRSPV QDHTSTN ^S TL vSNPATFPLN ATMYVDFSHD | |
| A. fumigatus 26906 | PAQGIGFTNE LIARLTRSPV QDHTSTN ^S TL vSNPATFPLN ATMYVDFSHD | |
| A. fumigatus 32239 | PAQGIGFTNE LIARLTNSPV QDHTSTN ^S TL DSDPATFPLN ATIYVDFSHD | |
| E. nidulans | PAQGIGFTNE LIARLTQSPV QDNTSTNHTL DSNPATFP ^L D rKLYADFSHD | |
| T. thermophilus | PAQGVGF ^V NE LIARMTHSPV QDYTTVNHTL DSNPATFPLN ATLYADFSHD | |
| M. thermophila | PTQGVGF ^V NE LLARLAgvPV RDgTSTNR ^T LD GDGP ^r TFPLG rPLYADFSHD | |
| Consensus | PAQGVGF-NE LIARLTHSPV QDHTSTNHTL DSNPATFPLN ATLYADFSHD | |
| Consensus phytase | PAQGVGFANE LIARLTRSPV QDHTSTNHTL DSNPATFPLN ATLYADFSHD | |
| | | |
| | 351 | 400 |
| A. terreus 9A-1 | SNLVSIFWAL GLYNGTAPLS qTSVESVSQT DGYAAAWTV ^P FAARAYVEMM | |
| A. terreus cbs | SNLVSIFWAL GLYNGT ^k PLS qTTVEDITrT DGYAAAWTV ^P FAARAYIEMM | |
| A. niger var. awamori | NGIISILFAL GLYNGT ^k PLS TTTVENITQT DGFS ^A WTVP FASR1YVEMM | |
| A. niger T213 | NGIISILFAL GLYNGT ^k PLS TTTVENITQT DGFS ^A WTVP FASR1YVEMM | |
| A. niger NRRL3135 | NGIISILFAL GLYNGT ^k PLS TTTVENITQT DGFS ^A WTVP FASR1YVEMM | |
| A. fumigatus 13073 | NSMVSIFFAL GLYNGTEPLS rTSVE ^S aKE1 DGYSASWVVP FGARAYF ^e T ^m | |
| A. fumigatus 32722 | NSMVSIFFAL GLYNGTG ^P LS rTSVE ^S aKE1 DGYSASWVVP FGARAYF ^e T ^m | |
| A. fumigatus 58128 | NSMVSIFFAL GLYNGTEPLS rTSVE ^S aKE1 DGYSASWVVP FGARAYF ^e T ^m | |
| A. fumigatus 26906 | NSMVSIFFAL GLYNGTEPLS rTSVE ^S aKE1 DGYSASWVVP FGARAYF ^e T ^m | |
| A. fumigatus 32239 | NSMVSIFFAL GLYNGTEPLS rTSVE ^S aKE1 DGYSASWVVP FGARAYF ^e T ^m | |
| E. nidulans | NGMIPIFFAM GLYNGTEPLS qTSeESTKES NGYSASWAVP FGARAYF ^e T ^m | |
| T. thermophilus | NSMISIFFAM GLYNGTQPLS mDSVESIQEm DGYAASWTVP FGARAYFELM | |
| M. thermophila | NTMTSIFaAL GLYNGTAKLS TTEIKSIEET DGYSAASWTVP FGGRAYIEMM | |
| | NDMMGV ^L gAL GaYDGVP ^P LD KTArrDpEE1 GGYAASWAVP FAARIYVEKM | |
| Consensus | NSMISIFFAL GLYNGTAPLS TTSVESIEET DGYAASWTVP FGARAYVEMM | |
| Consensus phytase | NSMISIFFAL GLYNGTAPLS TTSVESIEET DGYSASWTVP FGARAYVEMM | |
| | | |
| | 401 | 450 |
| A. terreus 9A-1 | QC..... RAEKE PLVRVLVNDR VMPLHGCPTD KLGRCKrDAF | |
| A. terreus cbs | QC..... RAEKQ PLVRVLVNDR VMPLHGC ^A VD NLGRCKrDDF | |
| A. niger var. awamori | QC..... QAEQE PLVRVLVNDR VVPLHGC ^P ID aLGRCTrDSF | |
| A. niger T213 | QC..... QAEQE PLVRVLVNDR VVPLHGC ^P ID aLGRCTrDSF | |
| A. niger NRRL3135 | QC..... QAEQE PLVRVLVNDR VVPLHGC ^P VD aLGRCTrDSF | |
| A. fumigatus 13073 | QC..... KSEKE PLVRALINDR VVPLHGC ^D VD KLGRCKLNDF | |
| A. fumigatus 32722 | QC..... KSEKE PLVRALINDR VVPLHGC ^D VD KLGRCKLNDF | |
| A. fumigatus 58128 | QC..... KSEKE SLVRALINDR VVPLHGC ^D VD KLGRCKLNDF | |
| A. fumigatus 26906 | QC..... KSEKE PLVRALINDR VVPLHGC ^D VD KLGRCKLNDF | |
| A. fumigatus 32239 | QC..... KSEKE PLVRALINDR VVPLHGC ^A VD KLGRCKLNDF | |
| E. nidulans | QC..... E.KE PLVRVLVNDR VVPLHGC ^A VD KFGRCTLDDW | |
| T. thermophilus | QC..... DDSDE PVVRVLVNDR VVPLHGCEVD SLGRCKrDDF | |
| M. thermophila | RCs9999999 ggegrQEKDE eMVRVLVNDR VMTL ^k GCGAD ErGMCTLErF | |
| Consensus | QC----- QAEKE PLVRVLVNDR VVPLHGC ^A VD KLGRCKLDDF | |
| Consensus phytase | QC..... QAEKE PLVRVLVNDR VVPLHGC ^A VD KLGRCKRDDF | |

| | 451 | 471 |
|-------------------------------------|------------|--------------|
| <i>A. terreus</i> 9A-1 | VAGLSFAQAG | GNWADCF~~~ ~ |
| <i>A. terreus</i> cbs | VEGLSFARAG | NWAECF~~~ |
| <i>A. niger</i> var. <i>awamori</i> | VrGLSFARSG | GDWAECsA~~ ~ |
| <i>A. niger</i> T213 | VrGLSFARSG | GDWAECFA~~ ~ |
| <i>A. niger</i> NRRL3135 | VrGLSFARSG | DWAECFA~~ |
| <i>A. fumigatus</i> 13073 | VKGLSWARSG | GNWGECFS~~ ~ |
| <i>A. fumigatus</i> 32722 | VKGLSWARSG | GNWGECFS~~ ~ |
| <i>A. fumigatus</i> 58128 | VKGLSWARSG | GNWGECFS~~ ~ |
| <i>A. fumigatus</i> 26906 | VKGLSWARSG | GNWGECFS~~ ~ |
| <i>A. fumigatus</i> 32239 | VKGLSWARSG | NSEQSFS~~ |
| <i>E. nidulans</i> | VEGLNFARSG | GNWkTCFTl~~ |
| <i>T. thermophilus</i> | VrGLSFARqG | GNWEGCYAas e |
| <i>M. thermophila</i> | IESMAFARGN | GKWD1CFA~~ ~ |
| Consensus | VEGLSFARSG | GNWAECFA-- - |
| Consensus phytase | VEGLSFARSG | GNWAECFA.. . |

0 9 4 6 6 2 6 6 " 0 1 2 6 6 0 0

Fig. 1d

CP-1
Eco RI M G V F V V L L S I A T L F G S T
TATATGAATTCATGGCGTGTCGTCGCTACTGTCCATTGCCACCTGTTGGTCCA
1 **ATATACTTAAGTACCCGACAAGCAGCACGATGACAGGTAACGGTGGAAACAAGCCAAGGT**

S G T A L G P R G N S H S C D T V D G G
CATCCGGTACCGCCTGGGTCCCTCGTGGTAATTCTCACTCTGTGACACTGTTGACCGGTG
61 **GTAGGCCATGGCGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGCCAC**

CP-2
CP-3
Y Q C F P E I S H L W G Q Y S P Y F S L
GTTACCAATGTTCCCAGAAATTCTCACTGTGGGTCAATACTCTCCATACTCTCTT
121 **CAATGGTTACAAAGGGCTTTAAAGAGTGAAACACCCCAGTTATGAGAGGTATGAAGAGAA**

E D E S A I S P D V P D D C R V T F V Q
TGGAAGACGAATCTGCTATTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTCGTC
181 **ACCTTCTGCTTAGACGATAAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAG**

CP-4
CP-5
V L S R H G A R Y P T S S K S K A Y S A
AAGTTTTGTCTAGACACGGTGCTAGATAACCAACTCTTCTAAGTCTAAGGCTTACTCTG
241 **TTCAAAACAGATCTGTGCCACGATCTATGGGTTGAAGAAGATTAGATTCCGAATGAGAC**

L I E A I Q K N A T A F K G K Y A F L K
CTTGATTGAAGCTATTCAAAGAACGCTACTGCTTCAGGGTAAGTACGCTTCTTGA
301 **GAAACTAACCTCGATAAGTTCTTGCATGACGAAAGTTCCATTATGCGAAAGAAACT**

CP-6
CP-7
T Y N Y T L G A D D L T P F G E N Q M V
AGACTTACAACACTACCTGGGTGCTGACGACTTGACTCCATTGGTGAAAACCAAATGG
361 **TCTGAATGTTGATGTGAAACCCACGACTGCTGAACGTAGGTAAGCCACTTTGGTTACC**

N S G I K F Y R R Y K A L A R K I V P F
TTAACTCTGGTATTAAGTTCTACAGAACGATACAAGGCTTGGCTAGAAAGATTGTTCCAT
421 **AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTCTAACAGGTA**

CP-8
CP-9
I R A S G S D R V I A S A E K F I E G F
TCATTAGAGCTTCTGGTTCTGACAGAGTTATTGCTCTGCTGAAAAGTTCATGAGGTT
481 **AGTAATCTCGAACGACCAAGACTGTCTAACGAAAGACGACTTTCAAGTAACCTCCAA**

Q S A K L A D P G S Q P H Q A S P V I D
TCCAATCTGCTAACGGTGGCTGACCCAGGTTCTAACCCACACCAAGCTTCTCCAGTTATTG
541 **AGGTTAGACGATTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTCAAGAGGTCAATAAC**

Fig. 2a

CP-10

V I I P E G S G Y N N T L D H G T C T A
 601 ACGTTATTATTCCAGAAGGATCAGGTTACAACAACTTGGACCACGGTACTTGACTG
 TGCAATAATAAGGTCTTCtAGgCCAATGTTGTTGAAACCTGGTGCATGAACATGAC 660

CP-11

F E D S E L G D D V E A N F T A L F A P
 661 CTTTCGAAGACTCTGAATTGGGTGACGACGTTGAAGCTAACCTCACTGCTTGCTCGCTC
 GAAAGCTTCTGAGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAG 720

CP-12

A I R A R L E A D L P G V T L T D E D V
 721 CAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTGACTGACGAAAGACG
 GTCGATAATCTCGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTTCTGC 780

CP-13

V Y L M D M C P F E T V A R T S D A T E
 781 TTGTTTACTTGATGGACATGTGTCATTGAAACTGTTGCTAGAACTTCTGACGCTACTG
 AACAAATGAACTACCTGTACACAGGTAAGCTTGACAACGATCTGAAGAGACTGCGATGAC 840

L S P F C A L F T H D E W R Q Y D Y L Q
 841 AATTGTCTCCATTCTGTGCTTGTTCACTCACGACCAATGGAGACAATACGACTACTTGC
 TTAACAGAGGTAAGACACGAAACAAGTGAGTGCTGCTTACCTCTGTTATGCTGATGAACG 900

CP-14

CP-15

S L G K Y Y G Y G A G N P L G P A Q G V
 901 AATCTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGTCCAGCTAAGGTG
 TTAGAAACCCATTGATGCCAATGCCACGACCATTGGTAACCCAGGTCGAGTTCCAC 960

G F A N E L I A R L T R S P V Q D H T S
 961 TTGGTTTCGCTAACGAAATTGATTGCTAGATTGACTAGATCTCAGTTCAAGACCACACTT
 AACCAAAGCGATTGCTTAACGATCTAACTGATCTAGAGGTCAAGTTCTGGTGTGAA 1020

CP-16

T N H T L D S N P A T F P L N A T L Y A
 1021 CTACTAACACACTTGGACTCTAACCCAGCTACTTCCCATTGAAACGCTACTTGTACG
 GATGATTGGTGTAAACCTGAGATTGGTCATGAAAGGGTAACCTGCGATGAAACATGC 1080

D F S H D N S M I S I F F A L G L Y N G
 1081 CTGACTTCTCTCACGACAACTCTATGATTCTATTTCCTCGCTTGGTTGTACAACG
 GACTGAAGAGAGTGCTGTTGAGATACTAAAGATAAAAGAAGCGAAACCCAAACATGTTGC 1140

CP-18

CP-19

T A P L S T T S V E S I E E T D G Y S A
 1141 GTACTGCTCCATTGCTACTACTTCTGTTGAATCTATTGAAAGAAACTGACGGTTACTCTG
 CATGACGAGGTAACAGATGATGAAGACAACCTAGATAACTTCTTGACTGCCAATGAGAC 1200

Fig. 2b

S W T V P F G A R A Y V E M M Q C Q A E
 CTTCTTGGACTGTTCCATTGGTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 GAAGAACCTGACAAGGTAAGCCACGATCTGAATGCAACTTACTACGTTACAGTTCGAC
 CP-20
 CP-21
 K E P L V R V L V N D R V V P L H G C A
 AAAAGGAACCATTGGTTAGAGTTGGTTAACGACAGAGTTGCACGGTTGTG
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320
 TTTTCCTTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC
 V D K L G R C K R D D F V E G L S F A R
 CTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTA
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380
 GACAACCTGTTCAACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGAT
 CP-22
 S G G N W A E C F A * Eco RI
 GATCTGGTGGTAACTGGGCTGAATGTTTCGCTTAAGAATTCTATA
 1381 -----+-----+-----+-----+-----+-----+-----+ 1426
 CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT

| | | | | |
|-----------------------------|--------------------|-------------------|-------------------|-------------------------------------|
| | | 1 | | 50 |
| <i>P. involutus</i> (phyA1) | SvP.KnTAPt | FPIPeSeQrn | WSPYSPYFPL | AeYkAPPAGC QInQVNIIQR |
| <i>P. involutus</i> (phyA2) | SvP.RniAPK | FSIPeSeQrn | WSPYSPYFPL | AeYkAPPAGC EInQVNIIQR |
| <i>T. pubescens</i> | hiPlRdTSAc | LdVTrDvQqs | WSmYSPYFPa | AtYvAPPASC QInQVHIIQR |
| <i>A. pediades</i> | GgvvQaTfvQ | pffPPpQiQds | WAAYTPYYPV | qaYtPPPkDC KItQVNIIQR |
| <i>P. lycii</i> | StQfsfvAAQ | LPIPaQnts | WGPYdPFFPV | EpYaAPPAGC tVtQVNLIQR |
| Basidio | S-P-R-TAAQ | LPIP-Q-Q-- | WSPYSPYFPV | A-Y-APPAGC QI-QVNIIQR |
| | | 51 | | 100 |
| <i>P. involutus</i> (phyA1) | HGARFPTSGA | TTRIKAGLTK | LQGvqnfTDA | KFNFIksfkY dLGnsDLVPF |
| <i>P. involutus</i> (phyA2) | HGARFPTSGA | ATRIKAGLSK | LQSvqnfTDP | KFDFlksfTY dLGtsDLVPF |
| <i>T. pubescens</i> | HGARFPTSGA | AkRIQTAVAK | LKAAsnyTDP | 1LAFVtNyTY sLGqDsLVeL |
| <i>A. pediades</i> | HGARFPTSGA | GTRIQAAVKK | LQSAktyTDP | RLDFLtNyTY tLGHDDLVPF |
| <i>P. lycii</i> | HGARWPTSGA | rSRqvAAVAK | IQmArpFTDP | KYEFLnDfvY kFGvADLLPF |
| Basidio | HGARFPTSGA | ATRIQAAVAK | LQSA---TDP | KLDFL-N-TY -LG-DDLVPF |
| | | 101 | | 150 |
| <i>P. involutus</i> (phyA1) | GAAQSfDAGQ | EAFARYSKLV | SkNNLPFIRA | dGSDRVVDSA TNWTAGFASA |
| <i>P. involutus</i> (phyA2) | GAAQSfDAG1 | EvFARYSKLV | SsDNLPFIRS | dGSDRVVDTA TNWTAGFASA |
| <i>T. pubescens</i> | GATQSSEAGQ | EAFTRYSSLV | SaDELPFVRA | SGSDRVVATA nNWTAGFALA |
| <i>A. pediades</i> | GALQSSQAGE | ETFqRYSFLV | SkeNLPFVRA | SSSNRVRVDSA TNWTEGFSAa |
| <i>P. lycii</i> | GAnQShQTGt | DmYTRYStLf | egGDVPFVRA | AGdQRVVDSS TNWTAGFGDa |
| Basidio | GA-QSSQAGQ | EAFTRYS-LV | S-DNLPFVRA | SGSDRVVDSA TNWTAGFA-A |
| | | 151 | | 200 |
| <i>P. involutus</i> (phyA1) | ShNTvqPkLn | LILPQtGNDT | LEDNMCPaAG | DSDPQvNaWL AVafPSITAR |
| <i>P. involutus</i> (phyA2) | SrNAiqPkLd | LILPQtGNDT | LEDNMCPaAG | ESDPQvDaWL AsafPSVTaQ |
| <i>T. pubescens</i> | SsNSitPvLs | VIISEaGNDT | LDDNMCPaAG | DSDPQvNqWL AqFAPPMTAR |
| <i>A. pediades</i> | ShHvlnPiLf | VILSEslNDT | LDDaMCPnAG | sSDPQtGiWt SIYGTPIANR |
| <i>P. lycii</i> | SgETvlpTlq | VVLqEeGNcT | LcNNMCPnEv | DGDest.tWL GVFAPnITAR |
| Basidio | S-NT--P-L- | VILSE-GNDT | LDDNMCP-AG | DSDPQ-N-WL AVFAPPITAR |
| | | 201 | | 250 |
| <i>P. involutus</i> (phyA1) | LNAAAAPSvNL | TDtDAfNLvs | LCAF1TVSkE | kkSdFCtlFE giPGsFeAFa |
| <i>P. involutus</i> (phyA2) | LNAAAAPGANL | TDaDAfNLvs | LCPFmTVSkE | qkSdFCtlFE giPGsFeAFa |
| <i>T. pubescens</i> | LNAGAPGANL | TdtDTyNLlt | LCPFETVAtE | rrSeFCDIYE elQAE.dAFa |
| <i>A. pediades</i> | LNqqAPGANI | TAadDvsNLip | LCAFETIVkE | tpSpFCNLF. .tPEEFaqFe |
| <i>P. lycii</i> | LNAAAAPSANL | SDsDALtLmd | MCPFDTLSsG | naSpFCDLF. .tAEEYvSYe |
| Basidio | LNAAAAPGANL | TD-DA-NL-- | LCPFETVS-E | --S-FCDLFE --PEEF-AF- |

Fig. 3a

| | | |
|-----------------------------|--|-----|
| | 251 | 300 |
| <i>P. involutus</i> (phyA1) | YgGDLDKFYG TGYYGQeLGPV QGVGYVNELI ARLTnsAVRD NTQTNRTLDA | |
| <i>P. involutus</i> (phyA2) | YaGDLDKFYG TGYYGQALGPV QGVGYINELL ARLTnsAVnD NTQTNRTLDA | |
| <i>T. pubescens</i> | YnADLDKFYG TGYYGQPLGPV QGVGYINELI ARLtaQnVsD HTQTNsTLDS | |
| <i>A. pediades</i> | YfGDLDKFYG TGYYGQPLGPV QGVGYINELL ARLtemPVRD NTQTNRTLDS | |
| <i>P. lycii</i> | YyyDLDKYYG TGpGNALGPV QGVGYVNELL ARLTgQAVRD ETQTNRTLDS | |
| Basidio | Y-GDLDKFYG TGYYGQPLGPV QGVGYINELL ARLT-QAVRD NTQTNRTLDS | |
| | 301 | 350 |
| <i>P. involutus</i> (phyA1) | SPvTFPLNKT FYADFSHDN1 MVAVFSAMGL FrQPAPLsts vPNPwRTWrT | |
| <i>P. involutus</i> (phyA2) | APdTTFPLNKT MYADFSHDN1 MVAVFSAMGL FrQSAPLsts tPDPNRTWLT | |
| <i>T. pubescens</i> | SPeTFPLNRT LYADFSHDNQ MVAIFSAMGL FNQSAPLDPT tPDPaRTFLv | |
| <i>A. pediades</i> | SP1TFPLDRS IYADLSHDNQ MIAIFSAMGL FNQSSPLDPS fPNPKRTWVT | |
| <i>P. lycii</i> | dPaTFPLNRT FYADFSHDNt MVPIFAALGL FNATA.LDPl kPDeNRlWvd | |
| Basidio | SP-TFPLNRT FYADFSHDNQ MVAIFSAMGL FNQSAPLDPS -PDPNRTWVT | |
| | 351 | 400 |
| <i>P. involutus</i> (phyA1) | SsLVPFSGRM VVERLsC..f GT..... tkv RVLVQDqVQP | |
| <i>P. involutus</i> (phyA2) | SsVVPFSARM aVERLsC..a GT..... tkv RVLVQDqVQP | |
| <i>T. pubescens</i> | KKIVPFSARM VVERLdC..g GA..... qsv RLLVNDAVQP | |
| <i>A. pediades</i> | SRLtPFSARM VtERL1Cqrd GTgsggpsri mrngnvqtfv RILVNDALQP | |
| <i>P. lycii</i> | SKLVPFSGHM tVEKlaC... sgkeav RVLVNDAVQP | |
| Basidio | SKLVPFSGARM VVERL-C--- GT----- v RVLVNDAVQP | |
| | 401 | 441 |
| <i>P. involutus</i> (phyA1) | LEFCGGDrNG 1CTLAKFVES QtFARsDGaG DFEKCFATSa ~ | |
| <i>P. involutus</i> (phyA2) | LEFCGGDqDG 1CALDkFVES QaYARsGGaG DFEKCLATTv ~ | |
| <i>T. pubescens</i> | LAFCGADtsG vCTLDAFVES QaYARNDGEG DFEKCFAT~~ ~ | |
| <i>A. pediades</i> | LKFCGGDmDS 1CTLEAFVES QkYAREDGQG DFEKCFD~~~ ~ | |
| <i>P. lycii</i> | LEFCGG.vDG vCeLsAFVES QTYARENGQQ DFAKCgfvpS e | |
| Basidio | LEFCGGD-DG -CTLDAFVES Q-YAREDGQQ DFEKCFATP- - | |

| | | | |
|-----------------------|--------------|------------|-----------------------|
| | | 1 | 50 |
| A. terreus 9a1 | KhsdCNSVDh | GYQCFPELSH | kWG1YAPYFS |
| A. terreus cbs | NhsdCtSVDr | GYQCFPELSH | kWG1YAPYFS |
| A. niger var. awamori | NqsTCDTVDq | GYQCFSETSH | LWGQYAPFFS |
| A. niger NRRL3135 | NqsSCDTVDq | GYQCFSETSH | LWGQYAPFFS |
| A. fumigatus 13073 | GSkSCDTVDl | GYQCSPATSH | LWGQYSPFFS |
| A. fumigatus 32722 | GSkSCDTVDl | GYQCSPATSH | LWGQYSPFFS |
| A. fumigatus 58128 | GSkSCDTVDl | GYQCSPATSH | LWGQYSPFFS |
| A. fumigatus 26906 | GSkSCDTVDl | GYQCSPATSH | LWGQYSPFFS |
| A. fumigatus 32239 | GSkACDTVEL | GYQCSPGTSH | LWGQYSPFFS |
| E. nidulans | QNHSCNTaDG | GYQCFPNVSH | VWGQYSPYFS |
| T. thermophilus | DShSCNTVEG | GYQCPEISH | sWGQYSPFFS |
| T. lanuginosus | ~~~~~ | ~~~~~ | ~~~~~ |
| M. thermophila | ESRPCDtpDl | GFQCgTAISH | FWGQYSPYFS |
| Basidio | xSxPxrxrtaAa | qLPipxQxqx | xWSPYSPYFP |
| | | | VAXyxA.... pPaGCQIxqv |
| Consensus | NSHSCDTVDG | GYQC-PEISH | LWGQYSPFFS |
| Fcp10 | NSHSCDTVDG | GYQCFPEISH | LADESAISPD |
| | | | VPKGCRVTFV |
| | | 51 | 100 |
| A. terreus 9a1 | QVLARHGARS | PThSKTKaYA | AtIaAIQKSA |
| A. terreus cbs | QVLARHGARS | PTdSKTKaYA | AtIaAIQKNA |
| A. niger var. awamori | QVLSRHGARY | PTeSKGKKYS | ALieEIQQNv |
| A. niger NRRL3135 | QVLSRHGARY | PTdSKGKKYS | ALieEIQQNA |
| A. fumigatus 13073 | QVLSRHGARY | PTSSKSKKYk | kLvtAIQaNA |
| A. fumigatus 32722 | QVLSRHGARY | PTSSKSKKYk | kLvtAIQaNA |
| A. fumigatus 58128 | QVLSRHGARY | PTSSKSKKYk | kLvtAIQaNA |
| A. fumigatus 26906 | QVLSRHGARY | PTSSKSKKYk | kLvtAIQaNA |
| A. fumigatus 32239 | QVLSRHGARY | PTASKSKKYk | kLvtAIQKNA |
| E. nidulans | QVLSRHGARY | PTeSKSKaYS | GLieAIQKNA |
| T. thermophilus | QLLSRHGARY | PTSSKTELYS | qLIsriIQkTA |
| T. lanuginosus | QVLSRHGARY | PTAhKSEvYA | ELLqrIQDta |
| M. thermophila | QVLSRHGARA | PTlkRAasYv | DLIdriIHhGA |
| Basidio | NIIqRHGARF | PTSGaAtRiq | AaVakLQsax |
| | | | xxtDPKLDfL xnxtYxLGxG |
| Consensus | QVLSRHGARY | PTSSKSKKYS | ALI-AIQKNA |
| Fcp10 | QVLSRHGARY | PTSSKSKKYS | ALIEAIQKNA |
| | | | TAFKGKYAFL KTNYNTLGAD |
| | | 101 | 150 |
| A. terreus 9a1 | ELTPFGrNQL | rD1GaQFYeR | YNAL.TRhIn |
| A. terreus cbs | NLTPFGrNQL | qD1GaQFYRR | YDTL.TRhIn |
| A. niger var. awamori | DLTPFGEQEL | VNSGIKFYQR | YESL.TRnII |
| A. niger NRRL3135 | DLTPFGEQEL | VNSGIKFYQR | YESL.TRnIV |
| A. fumigatus 13073 | DLTPFGEQQL | VNSGIKFYQR | YKAL.ARsVV |
| A. fumigatus 32722 | DLTPFGEQQL | VNSGIKFYQR | YKAL.ARsVV |
| A. fumigatus 58128 | DLTPFGEQQL | VNSGIKFYQR | YKAL.ARsVV |
| A. fumigatus 26906 | DLTAFGEQQL | VNSGIKFYQR | YKAL.ARsVV |
| A. fumigatus 32239 | DLTPFGEQQM | VNSGIKFYQR | YKAL.AgsVV |
| E. nidulans | DLTiFGENQM | VDSgaKFYRR | YKnL.ARknt |
| T. thermophilus | DLTPFGENQM | IQ1G1KFYnH | YKSL.ARnaV |
| T. lanuginosus | NLTRFGEQQM | MESGrQFYHR | YREq.ARIV |
| M. thermophila | ELTRtGQQQM | VNSGIKFYRR | YRAL.ARksI |
| Basidio | DLvPFGAxQs | sQAGqEaFtR | YsxLvSxdnL |
| | | | PFVRASGSDR VVDSatNWtA |
| Consensus | DLTPFGEQQM | VNSGIKFYRR | YKAL-AR-IV |
| Fcp10 | DLTPFGEQQM | VNSGIKFYRR | YKAL.ARkIV |
| | | | PFVRASGSDR VIASAEKFIE |

Fig. 4a

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| | | | |
|-------------------------------------|-------------|-------------|------------------------------------|
| | 151 | | 200 |
| A. <i>terreus</i> 9a1 | GFQATARqDDh | hAnphQPSPr | VDVaIPEGsA YNNNTLEHSLC TAFEs...St |
| A. <i>terreus</i> cbs | GFQNARqGDP | hAnphQPSPr | VDVVIPEGtA YNNNTLEHSIC TAFEA...St |
| A. <i>niger</i> var. <i>awamori</i> | GFQSTKLnDP | rAqpgQSSPk | IDVVISEAsS sNNNTLDpGtC TvFED...SE |
| A. <i>niger</i> NRRL3135 | GFQSTKLnDP | rAqpgQSSPk | IDVVISEAsS sNNNTLDpGtC TvFED...SE |
| A. <i>fumigatus</i> 13073 | GFQqAKLADP | gAt.nRAAPa | ISVIIPESeT FNNTLDHGVC TkFEa...SQ |
| A. <i>fumigatus</i> 32722 | GFQqAKLADP | gAt.nRAAPa | ISVIIPESeT FNNTLDHGVC TkFEa...SQ |
| A. <i>fumigatus</i> 58128 | GFQqAKLADP | gAt.nRAAPa | ISVIIPESeT FNNTLDHGVC TkFEa...SQ |
| A. <i>fumigatus</i> 26906 | GFQqAKLADP | gAt.nRAAPa | ISVIIPESeT FNNTLDHGVC TkFEa...SQ |
| A. <i>fumigatus</i> 32239 | GFQqANVADP | gAt.nRAAPV | ISVIIPESeT YNNNTLDHSVC TnFEa...SE |
| E. <i>nidulans</i> | GFRkAQLhDh | g.s.gQATPV | VNVIPIEidG FNNTLDHStC vSFen...dE |
| T. <i>thermophilus</i> | GFQSAKVLDP | hSdkhDAPPt | INVIIeEGpS YNNNTLDtGsC PvFEd...Ss |
| T. <i>lanuginosus</i> | GFQdAKdrDP | rSnkdQAePV | INVIISEEtG sNNNTLDgltC PAaEe...Ap |
| M. <i>thermophila</i> | GFHSALLADR | gStvrPTlPy | dmVVIPETaG aNNNTLHNLDLC TAFEegPySt |
| Basidio | GFaxA..... | sxnTxxPx | LxVILSExg. .NDTLDDNMc |
| Consensus | GFQSAKLADP | -A---QASPV | INVIIEEE-G YNNNTLDHGLC TAFE--P-SE |
| Fcp10 | GFQSAKLADP | GANPHQASPV | INVIIEEEAG YNNNTLDHGLC TAFEE...SE |
| | 201 | | 250 |
| A. <i>terreus</i> 9a1 | VGDDAvANFT | AVFAPAIaqR | LEAdLPGVQL StDDVVNLMA MCPFETVSLT |
| A. <i>terreus</i> cbs | VGDAaADNFT | AVFAPAIakR | LEAdLPGVQL SADDVVNLMA MCPFETVSLT |
| A. <i>niger</i> var. <i>awamori</i> | LADtVEANFT | AtFAPSIRqR | LendLSGVtL TDtEVtyLMD MCSFDTISTs |
| A. <i>niger</i> NRRL3135 | LADtVEANFT | AtFvPSIRqR | LendLSGVtL TDtEVtyLMD MCSFDTISTs |
| A. <i>fumigatus</i> 13073 | LGDEVAANFT | ALFAPDirAR | aEkhlPGVtL TDEDVVSLMD MCSFDTVarT |
| A. <i>fumigatus</i> 32722 | LGDEVAANFT | ALFAPDirAR | aEkhlPGVtL TDEDVVSLMD MCSFDTVarT |
| A. <i>fumigatus</i> 58128 | LGDEVAANFT | ALFAPDirAR | aEkhlPGVtL TDEDVVSLMD MCSFDTVarT |
| A. <i>fumigatus</i> 26906 | LGDEVAANFT | ALFAPDirAR | aKkhLPgvL TDEDVVSLMD MCSFDTVarT |
| A. <i>fumigatus</i> 32239 | LGDEVEANFT | ALFAPPAIRAR | IekhlPGVQL TDDDVVSLMD MCSFDTVarT |
| E. <i>nidulans</i> | rADEIEANFT | AIMGPPIRkr | LendLPGIKL TNENVlyLMD MCSFDTMArT |
| T. <i>thermophilus</i> | gGHDaQEKFa | kqFAPAIleK | IKDhLPgvDL AvsDVpyLMD LCPFETLArn |
| T. <i>lanuginosus</i> | .DptqpAEFl | qVFGPRVlkk | ItkhMPGVNL T1EDVp1FMD LCPFDTVGsd |
| M. <i>thermophila</i> | IGDDaQDty1 | StFAGPiTAR | VNaNLPGaNL TDADtValMD LCPFETVAsS |
| Basidio | dSDpqnxw1 | AVFAPPiTAR | LNaaaPGaNL TDxDaxNLxx LCPFETVS.. |
| Consensus | LGDDVEANFT | AVFAPPiRar | LEA-LPGVNL TDEDVVNLMD MCPFDTVA-T |
| Fcp10 | LGDDVEANFT | AVFAPPiRar | LEAHLPGVNL TDEDVVNLMD MCPFDTVART |
| | 251 | | 300 |
| A. <i>terreus</i> 9a1 | d..Aht.... |LSPF | CDLFtA..tE WtQYNYL1SL dKYyGYGGGN |
| A. <i>terreus</i> cbs | d..Aht.... |LSPF | CDLFtA..ae WtQYNYL1SL dKYyGYGGGN |
| A. <i>niger</i> var. <i>awamori</i> | Tv..DTK.... |LSPF | CDLFTH..de WiHYDYLQSL kKYyGHGAGN |
| A. <i>niger</i> NRRL3135 | Tv..DTK.... |LSPF | CDLFTH..de WiNYDYLQSL kKYyGHGAGN |
| A. <i>fumigatus</i> 13073 | SD..ASQ.... |LSPF | CQLFTH..ne WkKYNYLQSL gKYyGYGAGN |
| A. <i>fumigatus</i> 32722 | SD..ASQ.... |LSPF | CQLFTH..ne WkKYNYLQSL gKYyGYGAGN |
| A. <i>fumigatus</i> 58128 | SD..ASQ.... |LSPF | CQLFTH..ne WkKYNYLQSL gKYyGYGAGN |
| A. <i>fumigatus</i> 26906 | SD..ASQ.... |LSPF | CQLFTH..ne WkKYNYLQSL gKYyGYGAGN |
| A. <i>fumigatus</i> 32239 | AD..ASE.... |LSPF | CAIFTH..ne WkKYDYLQSL gKYyGYGAGN |
| E. <i>nidulans</i> | AH..GTE.... |LSPF | CAIFTE..ke WlQYDYLQSL SKYyGYGAGS |
| T. <i>thermophilus</i> | ht..DT.... |LSPF | CALstQ..eE WqaYDYYQSL gKYyGhGGGN |
| T. <i>lanuginosus</i> | PvlfPrQ.... |LSPF | CHLFTa..dD WmaYDYYyTL dKYySHGGGS |
| M. <i>thermophila</i> | SsdpATadag | ggnggrpLSPF | CrlFSE..se WraYDYLQSV gKYyGYGPgn |
| Basidio | | xexxSxF | CDLFexxpeE FxaFxYxgdL dKYyGtGyGQ |
| Consensus | SD..ATQ--- | -----LSPF | CDLFTH---E W-QYDYLQSL -KYyGYGAGN |
| Fcp10 | SD..ATQ.... |LSPF | CDLFTH..DE WIQYDYLQSL GKYyGYGAGN |

Fig. 4b

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| | | | | |
|-----------------------|------------|-----------------------|-----------------------|-----------------------|
| | | 301 | | 350 |
| A. terreus 9a1 | PLGPvQGVGW | aNELMARLTR | A. PVHDHTCv | NNTLDASPAT FPLNATLYAD |
| A. terreus cbs | PLGPvQGVGW | aNELIARLTR | S. PVHDHTCv | NNTLDANPAT FPLNATLYAD |
| A. niger var. awamori | PLGPTQGVGY | aNELIARLTH | S. PVHDDTSS | NHTLDSNPAT FPLNSTLYAD |
| A. niger NRRL3135 | PLGPTQGVGY | aNELIARLTH | S. PVHDDTSS | NHTLDSSPAT FPLNSTLYAD |
| A. fumigatus 13073 | PLGPAQGIGF | tNELIARLTR | S. PVQDHTST | NsTLvSNPAT FPLNATMYvD |
| A. fumigatus 32722 | PLGPAQGIGF | tNELIARLTR | S. PVQDHTST | NsTLvSNPAT FPLNATMYvD |
| A. fumigatus 58128 | PLGPAQGIGF | tNELIARLTR | S. PVQDHTST | NsTLvSNPAT FPLNATMYvD |
| A. fumigatus 26906 | PLGPAQGIGF | tNELIARLTR | S. PVQDHTST | NsTLvSNPAT FPLNATMYvD |
| A. fumigatus 32239 | PLGPAQGIGF | tNELIARLTN | S. PVQDHTST | NsTLDSDPAT FPLNATIYvD |
| E. nidulans | PLGPAQGIGF | tNELIARLTQ | S. PVQDNTST | NHTLDSNPAT FPLDrkLYAD |
| T. thermophilus | PLGPAQGVGF | vNELIARMTH | S. PVQDYTTv | NHTLDSNPAT FPLNATLYAD |
| T. lanuginosus | AFGPSRGVGF | vNELIARMTh | N1PVKDHTTv | NHTLDDNPET FPLDAvLYAD |
| M. thermophila | PLGPTQGVGF | vNELLARLA. | GvPVRDgTST | NRTLDGDPrT FPLGrPLYAD |
| Basidio | PLGPvQGVGY | iNELLARLTx | qa.VRDNTqT | NRTLDSSPxT FPLNrTFYAD |
| Consensus | PLGPAQGVGF | -NELIARLTH | S-PVQDHTST | NHTLDSNPAT FPLNATLYAD |
| Fcp10 | PLGPAQGVGF | VNELIARLTH | S.PVQDHTST | NHTLDSNPAT FPLNATLYAD |
| | | 351 | | 400 |
| A. terreus 9a1 | FSHDSnLVSI | FWALGLYNGT | aPLSqtSVE. | .SvsQTDGYA AAWTVFPAAR |
| A. terreus cbs | FSHDSnLVSI | FWALGLYNGT | kPLSqtTVE. | .ditrTDGYA AAWTVFPAAR |
| A. niger var. awamori | FSHDNGIISI | LFALGLYNGT | kPLSTTTVE. | .NitQTDGFS SAWTVFASR |
| A. niger NRRL3135 | FSHDNGIISI | LFALGLYNGT | kPLSTTTVE. | .NitQTDGFS SAWTVFASR |
| A. fumigatus 13073 | FSHDNSMVS1 | FFALGLYNGT | ePLSrTSVE. | .SaKE1DGYS ASWvVPFGAR |
| A. fumigatus 32722 | FSHDNSMVS1 | FFALGLYNGT | gPLSrTSVE. | .SaKE1DGYS ASWvVPFGAR |
| A. fumigatus 58128 | FSHDNSMVS1 | FFALGLYNGT | ePLSrTSVE. | .SaKE1DGYS ASWvVPFGAR |
| A. fumigatus 26906 | FSHDNSMVS1 | FFALGLYNGT | ePLSrTSVE. | .SaKE1DGYS ASWvVPFGAR |
| A. fumigatus 32239 | FSHDNGM1PI | FFAMGLYNGT | ePLSqtSeE. | .StKESNGYS ASWAVPFGAR |
| E. nidulans | FSHDNSMISI | FFAMGLYNGT | qPLSmtdSVE. | .SiQEmDGYA ASWTVFPGAR |
| T. thermophilus | FSHDNTMTSI | FaALGLYNGT | akLSTTeIK. | .SIEETDGYS AAWTVFPGGR |
| T. lanuginosus | FSHDNTMTGI | FsAMGLYNGT | kPLSTSkiQP | pTgAAADGYA ASWAVPFAAR |
| M. thermophila | FSHDNDMMGV | LgALGaYDGv | pPLdkTA..R | rdpEE1GGYA ASWAVPFAAR |
| Basidio | FSHDNgMVAI | FsAMGLFNqS | aPLdPSxpDP | nrt.....Wv Tsk1VPFsAR |
| Consensus | FSHDNTMVSI | FFALGLYNGT | -PLSTTSVEP | -S-EETDGYA ASWAVPFAAR |
| Fcp10 | FSHDNTMVSI | FFALGLYNGT | KPLSTTSVE. | .SIEETDGYS AAWTVFPGAR |
| | | 401 | | 450 |
| A. terreus 9a1 | AYVEMMQC.. | ra..... |EKEPL | VRVLVNDRVm PLHGCPtDKL |
| A. terreus cbs | AYIEMMQC.. | ra..... |EKQPL | VRVLVNDRVm PLHGCAVDNL |
| A. niger var. awamori | 1YVEMMQC.. | Qa..... |EQEPL | VRVLVNDRVV PLHGCPIDaL |
| A. niger NRRL3135 | 1YVEMMQC.. | Qa..... |EQEPL | VRVLVNDRVV PLHGCPVDaL |
| A. fumigatus 13073 | AYfEtMQC.. | Ks..... |EKEPL | VRaLINDRVV PLHGCDVDKL |
| A. fumigatus 32722 | AYfEtMQC.. | Ks..... |EKEPL | VRaLINDRVV PLHGCDVDKL |
| A. fumigatus 58128 | AYfEtMQC.. | Ks..... |EKESL | VRaLINDRVV PLHGCDVDKL |
| A. fumigatus 26906 | AYfEtMQC.. | Ks..... |EKEPL | VRaLINDRVV PLHGCDVDKL |
| A. fumigatus 32239 | AYfEtMQC.. | Ks..... |EKEPL | VRaLINDRVV PLHGCAVDKL |
| E. nidulans | AYFELMQC.. | E..... |KKEPL | VRVLVNDRVV PLHGCAVDKF |
| T. thermophilus | AYIEMMQC.. | Dd..... |sDEPV | VRVLVNDRVV PLHGCEVDSL |
| T. lanuginosus | AYVELLRC.. | Etetsseeee EG... | EDEPF | VRVLVNDRVV PLHGCrVDRW |
| M. thermophila | iYVEkMRC.. | sggggggggg EGrqeKDEeM | VRVLVNDRVm TLkGCGaDER | |
| Basidio | mvVERLxCxx | xgtxxxxxxxxx | xxxxxxxxxx | VRVLVNDaVq PLEfCGgDxd |
| Consensus | AYVEMMQC-- | E----- | EG---EKEPL | VRVLVNDRVV PLHGCGVDKL |
| Fcp10 | AYVEMMQC.. | EA..... |EKEPL | VRVLVNDRVV PLHGCGVDKL |

Fig. 4c

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| | 451 | 482 |
|-------------------------------------|--|-----|
| <i>A. terreus</i> 9a1 | GRCKrDAFVA GLSFAQAG.. GNWADCF~~~ ~~ | |
| <i>A. terreus</i> cbs | GRCKrDDFVE GLSFARAG.. GNWAECF~~~ ~~ | |
| <i>A. niger</i> var. <i>awamori</i> | GRCtrDsFVr GLSFARSG.. GDWAECsA~~~ ~~ | |
| <i>A. niger</i> NRRL3135 | GRCtrDsFVr GLSFARSG.. GDWAECFA~~~ ~~ | |
| <i>A. fumigatus</i> 13073 | GRCKlNDFVK GLSWARSG.. GNWGECFS~~~ ~~ | |
| <i>A. fumigatus</i> 32722 | GRCKlNDFVK GLSWARSG.. GNWGECFS~~~ ~~ | |
| <i>A. fumigatus</i> 58128 | GRCKlNDFVK GLSWARSG.. GNWGECFS~~~ ~~ | |
| <i>A. fumigatus</i> 26906 | GRCKlNDFVK GLSWARSG.. GNWGECFS~~~ ~~ | |
| <i>A. fumigatus</i> 32239 | GRCKlNDFVK GLSWARSG.. GNSEQSFS~~~ ~~ | |
| <i>E. nidulans</i> | GRCtlDDWVE GLNFARSG.. GNWKtCFTl~ ~~ | |
| <i>T. thermophilus</i> | GRCKrDDFVr GLSFARqG.. GNWEGCYAas e~ | |
| <i>T. lanuginosus</i> | GRCRrDEWIK GLTFARqG.. GHWDrCF~~~ ~~ | |
| <i>M. thermophila</i> | GmCtlErFIE SMAFARGN.. GKWD1CFA~~~ ~~ | |
| Basidio | GxCtlDAFVE SqxYAReDgq GDFEKCFAtp xx | |
| Consensus | GRCK-DDFVE GLSFARSG-- GNWEECFA-- ~~ | |
| Fcp10 | GRCKRDDFVE GLSFARSG.. GNWEECFA.. .. | |

DRAFT: 2023-01-20

Fig. 4d

CP-1
 ECO RI M G V F V V L L S I A T L F G S T 17
 TATATGAATTCATGGCGTGTCTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCA
 1 -----+-----+-----+-----+-----+-----+ + 60
 ATATACTTAAGTACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAGCCAAGGT
 S G T A L G P R G N S H S C D T V D G G 37
 CATCCGGTACCGCCTGGGTCTCGTGGTAATTCTCACTCTTGACACTGTGACGGTG
 61 -----+-----+-----+-----+-----+-----+ + 120
 GTAGGCCATGGCGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGCCAC
 CP-2
 CP-3.10
 Y Q C F P E I S H L W G Q Y S P F F S L 57
 GTTACCAATGTTCCCAGAAATTCTCACTTGTGGGTCAAAACTCTCCATTCTTCTCTT
 121 -----+-----+-----+-----+-----+-----+ + 180
 CAATGGTTACAAAGGGTCTTAAAGAGTGAAACACCCCAGTTATGAGAGGTAAGAAGAGAA
 A D E S A I S P D V P K G C R V T F V Q 77
 TGGCTGACGAATCTGCTATTTCTCCAGACGTTCCAAGGGTTGTAGAGTTACTTCGTT
 181 -----+-----+-----+-----+-----+-----+ + 240
 ACCGACTGCTTAGACGATAAAAGAGGTCTGCAAGGTTCCGACATCTCAATGAAAGCAAG
 CP-4.10
 CP-5.10
 V L S R H G A R Y P T S S K S K K Y S A 97
 AAGTTTGCTAGACACGGTGTAGATAACCCAACTTCTCTAAAGTCTAAGAAGTACTCTG
 241 -----+-----+-----+-----+-----+-----+ + 300
 TTCAAAACAGATCTGTGCCACGATCTATGGGTTGAAGAAGATTCAAGATTCTCATGAGAC
 L I E A I Q K N A T A F K G K Y A F L K 117
 CTTTGATTGAAGCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTTGA
 301 -----+-----+-----+-----+-----+-----+ + 360
 GAAACTAACCGATAAGTTCTTGCATGACGAAAGTTCCATTCAATGCGAAAGAAACT
 CP-6
 CP-7.10
 T Y N Y T L G A D D L T P F G E Q Q M V 137
 AGACTTACAACACTACACTTGGGTGCTGACGACTTGACTCCATTGGTGAACAAACAAATGG
 361 -----+-----+-----+-----+-----+-----+ + 420
 TCTGAATGTTGATGTGAAACCCACGACTGCTGAAC TGAGGTAAGCCACTTGTGTTACC
 N S G I K F Y R R Y K A L A R K I V P F 157
 TTAACTCTGGTATTAAAGTTCTACAGAACGATACAAGGCTTGGCTAGAAAGATTGTTCCAT
 421 -----+-----+-----+-----+-----+-----+ + 480
 AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATTTCTAACAGGTA
 CP-8.10
 CP-9.10
 V R A S G S D R V I A S A E K F I E G F 177
 TCGTTAGAGCTCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCAAGGTT
 481 -----+-----+-----+-----+-----+-----+ + 540
 AGCAATCTCGAAGACCAAGACTGTCTCAATAACGAAGACGACTTTCAAGTAACCTCCAA
 Q S A K L A D P G A N P H Q A S P V I N 197
 TCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTA
 541 -----+-----+-----+-----+-----+-----+ + 600
 AGGTTAGACGATTCAACCGACTGGGTCCACGATTGGGTGTGGTTGCGAACAGGGTCAATAAT

Fig. 5a

CP-10.10

CP-11.10

V I I P E G A G Y N N T L D H G L C T A 217
 ACGTTATTATTCCAGAAGGTGCTGGTTACAACAACTTGGACCACGGTTGTACTG
 601 -----+-----+-----+-----+-----+-----+ 660
TGCAATAATAAGGTCTTCCACGACCAATGTTGTTGAAACCTGGTGCAAACACATGAC

F E E S E L G D D V E A N F T A V F A P 237
 CTTTCGAAGAACATCTGAATTGGGTGACGACGTTGAAGCTAACCTCACTGCTGTTTCGCTC
 661 -----+-----+-----+-----+-----+-----+ 720
GAAAGCTTCTTAGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAG

CP-12.10

P I R A R L E A H L P G V N L T D E D V 257
 CACCTATTAGAGCTAGATTGAAAGCTCACCGCCAGGTGTTAACTTGACTGACGAAGACG
 721 -----+-----+-----+-----+-----+-----+ 780
GTGGATAATCTCGATCTAACCTTCGAGTGAACGGTCCACAAATTGAAC TGACTGCTTCTGC

CP-13.10

V N L M D M C P F D T V A R T S D A T Q 277
 TTGTTAACTTGATGGACATGTGTCCATTGACACTGTTGCTAGAACCTCTGACGCTACTC
 781 -----+-----+-----+-----+-----+-----+ 840
AACAATTGAAC TACCTGTACACAGGTAAGCTGTGACAACGATCTGAAGACTGCGATGAG

L S P F C D L F T H D E W I Q Y D Y L Q 297
 AATTGTCCTCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGC
 841 -----+-----+-----+-----+-----+-----+ 900
TTAACAGAGGTAAAGACACTGAACAAAGTGAGTGCTGCTTACCTAACGTTATGCTGATGAACG

CP-14.10

CP-15.10

S L G K Y Y G Y G A G N P L G P A Q G V 317
 AATCTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCAGCTCAAGGTG
 901 -----+-----+-----+-----+-----+-----+ 960
TTAGAAACCCATTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCAC

G F V N E L I A R L T H S P V Q D H T S 337
 TTGGTTTCGTTAACGAATTGATTGACTAGATTGACTCACTCTCAGTTCAAGACCACACTT
 961 -----+-----+-----+-----+-----+-----+ 1020
AACCAAAGCAATTGCTTAACTAACGATCTAACGACTGAGTGAGAGGTCAAGTTCTGGTGTGAA

CP-16.10

CP-17.10

T N H T L D S N P A T F P L N A T L Y A 357
 CTACTAACACACTTGGACTCTAACCCAGCTACTTCCCATTGAAACGCTACTTGTACG
 1021 -----+-----+-----+-----+-----+-----+ 1080
GATGATTGGTGTGAAACCTGAGATTGGGTCGATGAAAGGGTAACCTGCGATGAAACATGC

D F S H D N T M V S I F F A L G L Y N G 377
 CTGACTTCTCTCACGACAACTATGGTTCTATTCTCGCTTGGGTTGTACAACG
 1081 -----+-----+-----+-----+-----+-----+ 1140
GACTGAAGAGAGTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGC

CP-18.10

CP-19.10

T K P L S T T S V E S I E E T D G Y A A 397
 GTACTAACGCCATTGTCTACTACTTCTGTTGAATCTATTGAAAGAAACTGACGGTTACGCTG
 1141 -----+-----+-----+-----+-----+-----+ 1200
CATGATTGGTAACAGATGATGAAAGACAACCTAGATAACTTCTTTGACTGCCAATGCGAC

Fig. 5b

16/56

S W T V P F A A R A Y V E M M Q C E A E 417
 CTTCTGGACTGTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTG
 1201 -----+-----+-----+-----+-----+-----+ 1260
 GAAGAACCTGACAAGGTAAGCCACGATCTGAATGCAACTTACTACGTTACACTTCGAC
CP-20.10
CP-21.10
 K E P L V R V L V N D R V V P L H G C G 437
 AAAAGGAACCATTGGTTAGAGTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
 1261 -----+-----+-----+-----+-----+-----+ 1320
 TTTTCCTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

 V D K L G R C K R D D F V E G L S F A R 457
 GTGTTGACAAGTTGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTA
 1321 -----+-----+-----+-----+-----+-----+ 1380
 CACAACTGTTCAACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGAT
CP-22.10
 S G G N W E E C F A * Eco RI 467
 GATCTGGTGGTACTGGGAAGAATGTTCGCTTAAGAATTATATA
 1381 -----+-----+-----+-----+-----+-----+ 1426
 CTAGACCACCATTGACCCTTCTACAAAGCGAATTCTTAAGTATA

Fig. 5c

1

| | |
|--------------------------------------|---|
| <i>P. involutus</i> (<i>phyA1</i>) | ~F Pipe seqR nWSPYSPYFP LAEykA.... pPaGCQInqV |
| <i>P. involutus</i> (<i>phyA2</i>) | ~Fs ipe seqR nWSPYSPYFP LAEykA.... pPaGcEInqV |
| <i>T. pubescens</i> | ~LDvtRDVqQ sWSmYSPYFP aAtyvA.... pPaSCQInqV |
| <i>A. pediades</i> | ~pffpPQIqD swAAyTPYYP VqAyTP.... pPKDCKITqV |
| <i>P. lycii</i> | ~LPipAQnTs nWGPyDPFFP VEpyAA.... pPEGCtVTqV |
| <i>A. terreus</i> 9a1 | KhsdCNSVDh GYQCfPELSh kWG1YAPYFS LqDESPFP1D VPEDCHITFV |
| <i>A. terreus</i> cbs | NhsdCtSVDr GYQCfPELSh kWG1YAPYFS LqDESPFP1D VPDDCHITFV |
| <i>A. niger</i> var. <i>awamori</i> | NqsTCDTVdQ GYQCfSETSH LWGQYAPFFS LANESAlSPD VPaGCRVTFa |
| <i>A. niger</i> T213 | NqsSCDTVDq GYQCfSETSH LWGQYAPFFS LANESvISPD VPaGCRVTFa |
| <i>A. niger</i> NRRL3135 | NqsSCDTVDq GYQCfSETSH LWGQYAPFFS LANESvISPE VPaGCRVTFa |
| <i>A. fumigatus</i> ATCC13073 | GskSCDTVD1 GYQC s PatSH LWGQYSPFFS LEDElSVSSK LPKDCRITLV |
| <i>A. fumigatus</i> ATCC32722 | GskSCDTVD1 GYQC s PatSH LWGQYSPFFS LEDElSVSSK LPKDCRITLV |
| <i>A. fumigatus</i> ATCC58128 | GskSCDTVD1 GYQC s PatSH LWGQYSPFFS LEDElSVSSK LPKDCRITLV |
| <i>A. fumigatus</i> ATCC26906 | GskSCDTVD1 GYQC s PatSH LWGQYSPFFS LEDElSVSSK LPKDCRITLV |
| <i>A. fumigatus</i> ATCC32239 | GskACDTvel GYQC s PGtSH LWGQYSPFFS LEDElSVSSD LPKDCRVTfV |
| <i>E. nidulans</i> | QNHSCNTaDg GYQC f PNVSh VWGQYSPYFS IEQESAISED VPhGCeVTFV |
| <i>T. thermophilus</i> | DShSCNTVEg GYQC r PEISH swGQYSPFFS LADQSEISPD VPQNCKITFV |
| <i>T. lanuginosus</i> | ~~~~~ ~~~nvDIAR hWGQYSPFFS LAEvSEISPA VPKGCRVeFV |
| <i>M. thermophila</i> | ESRPCDTpD1 GFQCgTAISH FWGQYSPYFS VPsElDaS.. IPDDCeVTFa |

Consensus Seq. 11 NSHSCDTVD- GYQC-PEISH LWGQYSPFFS LADESAISPD VPKGCRVTfV

51

| | |
|--------------------------------------|---|
| <i>P. involutus</i> (<i>phyA1</i>) | NIIqRHGARF PTSGaTTrIk AgL t KLQgvq nftDAKFnFI KSFKYdLGns |
| <i>P. involutus</i> (<i>phyA2</i>) | NIIqRHGARF PTSGa t Rik AgL s KLQsvq nftDPKFDFI KSFTydlGts |
| <i>T. pubescens</i> | HIIqRHGARF PTSGaAKRiq TaVAKLKaAS nyTDPLAFV tnYtYSLGqD |
| <i>A. pediades</i> | NIIqRHGARF PTSGaGtRiq AaVKKLQsak TytDPRLDfL tnYtYTLGhD |
| <i>P. lycii</i> | NLIqRHGARW PTSGarsRqv AaVAKIQmar PftDPKYEF L NdFvYkFGvA |
| <i>A. terreus</i> 9a1 | QVLARHGARS PThSKTKaYA AtIAaI Q KSA TaFpGKYAFL QSYNYSLDSE |
| <i>A. terreus</i> cbs | QVLARHGARS PTdSKTKaYA AtIAaI Q KNA TaLpGKYAFL KSYNYSMGSE |
| <i>A. niger</i> var. <i>awamori</i> | QVLSRHGARY PTeSKGKKYS ALIEeIQQNv TtFDGKYAFL KTNYNSLGAD |
| <i>A. niger</i> T213 | QVLSRHGARY PTeSKGKKYS ALIEeIQQNv TtFDGKYAFL KTNYNSLGAD |
| <i>A. niger</i> NRRL3135 | QVLSRHGARY PTdSKGKKYS ALIEeIQQNA TtFDGKYAFL KTNYNSLGAD |
| <i>A. fumigatus</i> ATCC13073 | QVLSRHGARY PTSSKSKY k kLvtaiQaNA TdFKGKFAFL KTNYNTLGAD |
| <i>A. fumigatus</i> ATCC32722 | QVLSRHGARY PTSSKSKY k kLvtaiQaNA TdFKGKFAFL KTNYNTLGAD |
| <i>A. fumigatus</i> ATCC58128 | QVLSRHGARY PTSSKSKY k kLvtaiQaNA TdFKGKFAFL KTNYNTLGAD |
| <i>A. fumigatus</i> ATCC26906 | QVLSRHGARY PTASKSKY k kLvtaiIQKNA TeFKGKFAFL ETNYNTLGAD |
| <i>A. fumigatus</i> ATCC32239 | QVLSRHGARY PTeSKSKaYS GLIEaI Q KNA TsFwGQYAF L ESYNYSLGAD |
| <i>E. nidulans</i> | QLLSRHGARY PTSSKTELYS qLi s RIQKtA TaYKGyYAF L KdYrYqLGAn |
| <i>T. thermophilus</i> | QVLSRHGARY PTAhKSEvYA ELLQRIQDtA TeFKGDFAF L RdYayhLGAD |
| <i>T. lanuginosus</i> | QVLSRHGARA PTlkRAasYv DLIDRIHhGA isYgPgYEFL RTYDYTLGAD |

Consensus Seq. 11 QVLSRHGARY PTSSKSKY~~s~~ ALIE~~RI~~QKNA T-FKGKYAFL KTNYNTLGAD

| | | |
|--------------------------------------|-------------|---|
| | 101 | |
| <i>P. involutus</i> (<i>phyA1</i>) | DLvPFGAAaQs | fDAGqEaFaR YskLvSKNnL PFIRAdGSDR VVDSATNWtA |
| <i>P. involutus</i> (<i>phyA2</i>) | DLvPFGAAaQs | fDAGLEVFaR YskLvSsDnL PFIRSdGSDR VVDTATNWtA |
| <i>T. pubescens</i> | SLveLGAtQs | sEAGqEaFtR YsSLvSaDeL PFVRASGSDR VVATANNWtA |
| <i>A. pediades</i> | DLvPFGA1Qs | sQAGeEtFQR YsfLvSKEnL PFVRASSSNR VVDSATNWtE |
| <i>P. lycii</i> | DLL1PFGANQs | hQTGtDMYtR YsTlfEgGdV PFVRAAGdQR VVDSStNWtA |
| <i>A. terreus</i> 9a1 | ELTPFGrNQL | rD1GaQFYeR YNAL.TRHIn PFVRATDAsR VhESAekFVE |
| <i>A. terreus</i> cbs | NLTPFGrNQL | qD1GaQFYRR YDTL.TRHIn PFVRAADssR VhESAekFVE |
| <i>A. niger</i> var. <i>awamori</i> | DLTPFGEQEL | VNSGIKFYQR YESL.TRNII PFIRSSGssR VIASGEKFIE |
| <i>A. niger</i> T213 | DLTPFGEQEL | VNSGIKFYQR YESL.TRNII PFIRSSGssR VIASGEKFIE |
| <i>A. niger</i> NRRL3135 | DLTPFGEQEL | VNSGIKFYQR YESL.TRNIV PFIRSSGssR VIASGKKFIE |
| <i>A. fumigatus</i> ATCC13073 | DLTPFGEQQL | VNSGIKFYQR YKAL.ARSVV PFIRASGSDR VIASGEKFIE |
| <i>A. fumigatus</i> ATCC32722 | DLTPFGEQQL | VNSGIKFYQR YKAL.ARSVV PFIRASGSDR VIASGEKFIE |
| <i>A. fumigatus</i> ATCC58128 | DLTPFGEQQL | VNSGIKFYQR YKAL.ARSVV PFIRASGSDR VIASGEKFIE |
| <i>A. fumigatus</i> ATCC26906 | DLTAFGEQQL | VNSGIKFYQR YKAL.ARSVV PFIRASGSDR VIASGEKFIE |
| <i>A. fumigatus</i> ATCC32239 | DLTPFGEQQM | VNSGIKFYQK YKAL.AgSvv PFIRSSGSDR VIASGEKFIE |
| <i>E. nidulans</i> | DLTiFGENQM | VDSaKaFYRR YKnL.ARknt PFIRASGSDR VVASAEKFIN |
| <i>T. thermophilus</i> | DLTPFGENQM | IQ1GIKFYnh YKSL.ARNaV PFVRCSGSDR VIASGr1FIE |
| <i>T. lanuginosus</i> | | NLTRFGEQQM MESGrQFYHR YREQ.AREIV PFVRAAGSAR VIASAEffNnr |
| <i>M. thermophila</i> | ELTRtGQQQM | VNSGIKFYRR YRAL.ARksI PFVRTAGqDR VvhSAENftQ |
| Consensus Seq. 11 | | DLTPFGENQM VNSGIKFYRR YKAL-ARNIV PFVRASGSDR VIASAEKFIE |
| | 151 | |
| <i>P. involutus</i> (<i>phyA1</i>) | GFaSA..... | shNtvqPk LNLILPQ..T gNDTLEDNMC PAaGD..... |
| <i>P. involutus</i> (<i>phyA2</i>) | GFaSA..... | srNaiqPk LDLILPQ..T gNDTLEDNMC PAaGE..... |
| <i>T. pubescens</i> | GFaLA..... | ssNsitPV LSVIISE..A gNDTLDDNNMC PAaGD..... |
| <i>A. pediades</i> | GFSAA..... | shHv1NP1 LfVILSE..S LNDTLDDAMC PnaGs..... |
| <i>P. lycii</i> | GFgdA..... | sgEtvlPt LQVVLQE..E gNctLCNNMC PnevD..... |
| <i>A. terreus</i> 9a1 | GFQTARqDDh | hAnpHQPSPr DVaIPEGSA YNNNTLEHSLC TAFEs...ST |
| <i>A. terreus</i> cbs | GFQNARqGDP | hAnpHQPSPr DVVVIPEGTA YNNNTLEHSIC TafeA...ST |
| <i>A. niger</i> var. <i>awamori</i> | GFQSTKLkDP | rAqpgQSSPk IDVVISEASS SNNTLDpGtC TvFED...Se |
| <i>A. niger</i> T213 | GFQSTKLkDP | rAqpgQSSPk IDVVISEASS SNNTLDpGtC TvFED...Se |
| <i>A. niger</i> NRRL3135 | GFQSTKLkDP | rAqpgQSSPk IDVVISEASS SNNTLDpGtC TvFED...Se |
| <i>A. fumigatus</i> ATCC13073 | GFQqAKLADP | gAt.NRAAPa ISVIIPESeT FNNNTLDHGVC TkFEA...Sq |
| <i>A. fumigatus</i> ATCC32722 | GFQqAKLADP | gAt.NRAAPa ISVIIPESeT FNNNTLDHGVC TkFEA...Sq |
| <i>A. fumigatus</i> ATCC58128 | GFQqAKLADP | gAt.NRAAPa ISVIIPESeT FNNNTLDHGVC TkFEA...Sq |
| <i>A. fumigatus</i> ATCC26906 | GFQqAKLADP | gAt.NRAAPV ISVIIPESeT YNNNTLDHSVC TnFEA...Se |
| <i>A. fumigatus</i> ATCC32239 | GFQqANVADP | gAt.NRAAPV ISVIIPESeT YNNNTLDHSVC TnFEA...Se |
| <i>E. nidulans</i> | GFRkAQhDh | g.s.gQATPV VNVIIPExidG FNNNTLDhstC vSFEN...de |
| <i>T. thermophilus</i> | GFQSAKVLDP | hSDKHDAPPt INVIIeEGPS YNNNTLDtGsC PvFED...SS |
| <i>T. lanuginosus</i> | GFQdAKdrDP | rSnkDQaEPV INVIISEETG sNNNTLDgltC PAaEE...AP |
| <i>M. thermophila</i> | GFHSALLADR | gStvRPTlPy dmVVIPETAG aNNNTLHNDLC TAFEEgpyST |
| Consensus Seq. 11 | | GFQSAKLDp -A--HQASPV INVIIPEGSG YNNNTLDHGLC TAFED---ST |
| | 200 | |

Fig. 6b

| | | |
|--------------------------------------|---|-----|
| | 201 | 250 |
| <i>P. involutus</i> (<i>phyA1</i>) | .SDpqvnaWl AVafPSItAR LNaaaPSVNL TDtDafNLVs LCAF1TVSK. | |
| <i>P. involutus</i> (<i>phyA2</i>) | .SDpqvDaWl AsafPSVtAQ LNaaaPGaNL TDADafNLVs LCPFmTVSK. | |
| <i>T. pubescens</i> | .SDpqvnQWl AqFAPPMtAR LNAGaPGaNL TDtDtyNLLt LCPFETVAt. | |
| <i>A. pediades</i> | .SDpqtGiWT SIYGTPIanR LNqqaPGaNI TAADVsnLIP LCAFETiV.K. | |
| <i>P. lycii</i> | .GDEST.tWl GVFApniTAR LNaaaPSaNL SDsDaLtLMD MCPFDTLss. | |
| <i>A. terreus</i> 9a1 | VGDDAvANFT AVFAPAlaqR LEADLPGVQL StDDVVNLMA MCPFETVSlT | |
| <i>A. terreus</i> cbs | VGDAADNFt AVFAPAlakR LEADLPGVQL SADDVVNLMA MCPFETVSlT | |
| <i>A. niger</i> var. <i>awamori</i> | LADtvEANFT AtFAPSIRqR LEndlSGVtL TDtEVtyLMD MCSFDTIStS | |
| <i>A. niger</i> T213 | LADtvEANFT AtFAPSIRqR LEndlSGVtL TDtEVtyLMD MCSFDTIStS | |
| <i>A. niger</i> NRRL3135 | LADtvEANFT AtFvPSIRqR LEndlSGVtL TDtEVtyLMD MCSFDTIStS | |
| <i>A. fumigatus</i> ATCC13073 | LGDevAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSIMD MCSFDTVART | |
| <i>A. fumigatus</i> ATCC32722 | LGDevAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSIMD MCSFDTVART | |
| <i>A. fumigatus</i> ATCC58128 | LGDevAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSIMD MCSFDTVART | |
| <i>A. fumigatus</i> ATCC26906 | LGDevAANFT ALFAPdIRAR aKkhLPGVtL TDEDVVSIMD MCSFDTVART | |
| <i>A. fumigatus</i> ATCC32239 | LGDevEANFT ALFAPAIRAR IEkhLPGVQL TDDDVVSIMD MCSFDTVART | |
| <i>E. nidulans</i> | rADEiEANFT AIMGPPIRkR LEndlPGIKL TNENVIyLMD MCSFDTMART | |
| <i>T. thermophilus</i> | GGHDAQEKFkA kqFAPAlIEk IKdhLPGVDL AvsDVpyLMD LCPFETLARn | |
| <i>T. lanuginosus</i> | .DptqpAEFl qVFGPRV1kK ItkhMPGVNL TLEDVp1FMD LCPFDTVGsd | |
| <i>M. thermophila</i> | IGDDAQDty1 StFAGPitAR VNanLPGaNL TDADtVaLMD LCPFETVASS | |
| Consensus Seq. 11 | LGDDAEANFT AVFAPPIRAR LEA-LPGVNL TDEDVVNLMD MCPFDTVART | |
| | | 300 |
| <i>P. involutus</i> (<i>phyA1</i>) | ekkSdF CtLFegiPGs FeaFAYggdL dKFYGtGyGQ | |
| <i>P. involutus</i> (<i>phyA2</i>) | eqkSdF CtLFegiPGs FeaFAYagdL dKFYGtGyGQ | |
| <i>T. pubescens</i> | errSeF CDIYeelqAE .daFAYnadL dKFYGtGyGQ | |
| <i>A. pediades</i> | etpSPF CNLF..TPEE FaQFEYFgdl dKFYGtGyGQ | |
| <i>P. lycii</i> | gnaSPF CDLF..TAEE YvsYBYYydl dKYyGtGPGN | |
| <i>A. terreus</i> 9a1 | dD..Aht.... LSPF CDLF..TATE WtQNYLLSL dKYyGyGGGN | |
| <i>A. terreus</i> cbs | dD..Aht.... LSPF CDLF..TAAE WtQNYLLSL dKYyGyGGGN | |
| <i>A. niger</i> var. <i>awamori</i> | Tv..DTK.... LSPF CDLF..ThDE WiHYDYLQSL kKYyGHGAGN | |
| <i>A. niger</i> T213 | Tv..DTK.... LSPF CDLF..ThDE WiHYDYLRSL kKYyGHGAGN | |
| <i>A. niger</i> NRRL3135 | Tv..DTK.... LSPF CDLF..ThDE WiNYDYLQSL kKYyGHGAGN | |
| <i>A. fumigatus</i> ATCC13073 | SD..ASQ.... LSPF CQLF..ThNE WkKYNYLQSL gKYyGYGAGN | |
| <i>A. fumigatus</i> ATCC32722 | SD..ASQ.... LSPF CQLF..ThNE WkKYNYLQSL gKYyGYGAGN | |
| <i>A. fumigatus</i> ATCC58128 | SD..ASQ.... LSPF CQLF..ThNE WkKYNYLQSL gKYyGYGAGN | |
| <i>A. fumigatus</i> ATCC26906 | SD..ASQ.... LSPF CQLF..ThNE WkKYNYLQSL gKYyGYGAGN | |
| <i>A. fumigatus</i> ATCC32239 | AD..ASE.... LSPF CAIF..ThNE WkKYDYLQSL gKYyGYGAGN | |
| <i>E. nidulans</i> | AH..GTE.... LSPF CAIF..TEKE WlQYDYLQSL SKYYGYGAGS | |
| <i>T. thermophilus</i> | ht..DT.... LSPF CALs..TqEE WqayDYYQSL gKYyGnGGGN | |
| <i>T. lanuginosus</i> | PvlfPrQ.... LSPF CHLF..TADD WmaYDYYyTL dKYySHGGGS | |
| <i>M. thermophila</i> | SsdpATadag ggngrplSPF CrLF..SEsE WraYDYLQSV gKYyGYGAGN | |
| Consensus Seq. 11 | SD--ATQ--- -----LSPF CDLF--TADE W-QYDYLQSL -KYyGYGAGN | |

Fig. 6c

| | | |
|--------------------------------------|---|-----|
| | 301 | 350 |
| <i>P. involutus</i> (<i>phyA1</i>) | elGPvQGVGY vNELIARLTN S.AVRDNTqT NRTLDASPVT FPLNKTFYAD | |
| <i>P. involutus</i> (<i>phyA2</i>) | ALGPvQGVGY iNELIARLTN S.AVNDNTqT NRTLDAA PDT FPLNKTFYAD | |
| <i>T. pubescens</i> | PLGPvQGVGY iNELIARLTa q.nVsDHTqT NsTLDSSPET FPLNrTLYAD | |
| <i>A. pediades</i> | PLGPvQGVGY iNELIARLTH m.PVRDNTqT NRTLDSSP1T FPLDrSIYAD | |
| <i>P. lycii</i> | ALGPvQGVGY vNELIARLTg q.AVRDETqT NRTLDSDPAT FPLNrTLYAD | |
| <i>A. terreus</i> 9a1 | PLGPvQGVGW aNELIARLTR A.PVHDHTCv NNTLDASPAT FPLNATLYAD | |
| <i>A. terreus</i> cbs | PLGPvQGVGW aNELIARLTR S.PVHDHTCv NNTLDANPAT FPLNATLYAD | |
| <i>A. niger</i> var. <i>awamori</i> | PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSNPAT FPLNSTLYAD | |
| <i>A. niger</i> T213 | PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSNPAT FPLNSTLYAD | |
| <i>A. niger</i> NRRL3135 | PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSSPAT FPLNSTLYAD | |
| <i>A. fumigatus</i> ATCC13073 | PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTlvSNPAT FPLNATMYvD | |
| <i>A. fumigatus</i> ATCC32722 | PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTlvSNPAT FPLNATMYvD | |
| <i>A. fumigatus</i> ATCC58128 | PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTlvSNPAT FPLNATMYvD | |
| <i>A. fumigatus</i> ATCC26906 | PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTlvSNPAT FPLNATMYvD | |
| <i>A. fumigatus</i> ATCC32239 | PLGPAQGIGF tNELIARLTN S.PVQDHTST NSTLDSDPAT FPLNATIYvD | |
| <i>E. nidulans</i> | PLGPAQGIGF tNELIARLTQ S.PVQDNTST NHTLDSNPAT FPLDyKLYAD | |
| <i>T. thermophilus</i> | PLGPAQGVGF vNELIARMTH S.PVQDYTTv NHTLDSNPAT FPLNATLYAD | |
| <i>T. lanuginosus</i> | AFGPSRGVGF vNELIARMTh N1PVKDHTTv NHTLDDNPET FPLDAvLYAD | |
| <i>M. thermophila</i> | PLGPTQGVGF vNELIARLA. GvPVRDgTST NRTLDGDPrT FPLGrPLYAD | |
| Consensus Seq. 11 | PLGPAQGVGF -NELIARLTH S-PVQDHTST NHTLDSNPAT FPLNATLYAD | |
| | | 400 |
| <i>P. involutus</i> (<i>phyA1</i>) | FSHDN1MVAV FsAMGLFrqP aPLSTSvpNP wrt.....Wr TSSLVPFSGR | |
| <i>P. involutus</i> (<i>phyA2</i>) | FSHDN1MVAV FsAMGLFrqS aPLSTStpDP nrt.....Wl TSSvVPFSAR | |
| <i>T. pubescens</i> | FSHDNqMVAI FsAMGLFNqS aPLdPTTpDP art.....Fl vkkivPFSAR | |
| <i>A. pediades</i> | LSHDNqMIAI FsAMGLFNqS sPLdPSfpNP krt.....Wv TSRLtpFSAR | |
| <i>P. lycii</i> | FSHDNTMVPI FaALGLFNAT a.LdPlkpDe nrl.....Wv DSK1VPFSGH | |
| <i>A. terreus</i> 9a1 | FSHDSnLVSI FWALGLYNGT aPLSqTSVES Vs..QTDGYA AAUTVPFAAR | |
| <i>A. terreus</i> cbs | FSHDSnLVSI FWALGLYNGT KPLSqTTVED It..rTDGYA AAUTVPFAAR | |
| <i>A. niger</i> var. <i>awamori</i> | FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR | |
| <i>A. niger</i> T213 | FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR | |
| <i>A. niger</i> NRRL3135 | FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR | |
| <i>A. fumigatus</i> ATCC13073 | FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..E1DGYS ASWvVPFGAR | |
| <i>A. fumigatus</i> ATCC32722 | FSHDNSMVSI FFALGLYNGT gPLSrTSVES ak..E1DGYS ASWvVPFGAR | |
| <i>A. fumigatus</i> ATCC58128 | FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..E1DGYS ASWvVPFGAR | |
| <i>A. fumigatus</i> ATCC26906 | FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..E1DGYS ASWvVPFGAR | |
| <i>A. fumigatus</i> ATCC32239 | FSHDNGM1PI FFAMGLYNGT EPLSqTSeES tk..ESNGYS ASWAVPFGAR | |
| <i>E. nidulans</i> | FSHDNSMISI FFAMGLYNGT QPLSmDSVES Iq..EmDGYS ASWTVPGAR | |
| <i>T. thermophilus</i> | FSHDNTM1SI FaALGLYNGT akLSTTeIKS Ie..ETDGYS AAWTVPFGGR | |
| <i>T. lanuginosus</i> | FSHDNTM1GI FsAMGLYNGT KPLSTSkiQP ptgaAADGYA ASWTVPFASR | |
| <i>M. thermophila</i> | FSHDNdMMGV LgALGaYDGv pPLdkTArrd ..peElGGYA ASWAVPFAAR | |
| Consensus Seq. 11 | FSHDNTM1VI FFALGLYNGT KPLSTTSVES I---ETDGYS ASWTVPGGR | |

Fig. 6d

| | | |
|-------------------------------------|--|------------------------------|
| | 401 | 450 |
| <i>P. involutus</i> (phyA1) | mvVERLsC.. fGt..... | Tk VRVLVQDQVq PLEfCGgDRn |
| <i>P. involutus</i> (phyA2) | maVERLsC.. AGt..... | Tk VRVLVQDQVq PLEfCGgDQd |
| <i>T. pubescens</i> | mvVERLDC.. GGa..... | Qs VRLLVNDAvq PLafCGaDts |
| <i>A. pediades</i> | mvtErLlCQr DGtGsGGpsr imrNgnvQTF | VRILVNDAlq PLkfCGgDmd |
| <i>P. lycii</i> | mtVEkLaC.. sgKea | VRVLVNDAvq PLEfCGg.vd |
| <i>A. terreus</i> 9a1 | AYVEMMQCrA EK . . . EPL | VRVLVNDRVM PLHGCPtDKL |
| <i>A. terreus</i> cbs | AYIEMMQCrA EK . . . QPL | VRVLVNDRVM PLHGCAVDNL |
| <i>A. niger</i> var. <i>awamori</i> | LYVEMMQCQA EQ . . . EPL | VRVLVNDRVV PLHGCPIDaL |
| <i>A. niger</i> T213 | LYVEMMQCQA EQ . . . EPL | VRVLVNDRVV PLHGCPIDaL |
| <i>A. niger</i> NRRL3135 | LYVEMMQCQA EQ . . . EPL | VRVLVNDRVV PLHGCPVDaL |
| <i>A. fumigatus</i> ATCC13073 | AYfEtMQCKS EK . . . EPL | VRaLINDRvv PLHGCDVDKL |
| <i>A. fumigatus</i> ATCC32722 | AYfEtMQCKS EK . . . EPL | VRaLINDRvv PLHGCDVDKL |
| <i>A. fumigatus</i> ATCC58128 | AYfEtMQCKS EK . . . ESL | VRaLINDRvv PLHGCDVDKL |
| <i>A. fumigatus</i> ATCC26906 | AYfEtMQCKS EK . . . EPL | VRaLINDRvv PLHGCDVDKL |
| <i>A. fumigatus</i> ATCC32239 | AYfEtMQCKS EK . . . EPL | VRaLINDRvv PLHGCAVDKL |
| <i>E. nidulans</i> | AYfELMQCE. KK . . . EPL | VRVLVNDRVV PLHGCAVDKF |
| <i>T. thermophilus</i> | AYIEMMQCDD SD . . . EPV | VRVLVNDRVV PLHGCEVDSL |
| <i>T. lanuginosus</i> | AYVELLRCET ETsSeEEeEG .. ED . . . EPF | VRVLVNDRVV PLHGCrVDRW |
| <i>M. thermophila</i> | iYVEkMRCsG GGgGgGGgEG .. rQekdEeM | VRVLVNDRVM TLkGCGaDER |
| Consensus Seq. 11 | AYVEMMQCEA GG-G-GG-EG --EK---EPL | VRVLVNDRVV PLHGCGVDKL |
| | 451 | 482 |
| <i>P. involutus</i> (phyA1) | G1CtLAKFVE SqTFARSDga GDFEKCFAts a- | |
| <i>P. involutus</i> (phyA2) | G1CaLDKFVE SqAYARSGga GDFEKCLAtt v- | |
| <i>T. pubescens</i> | GvCtLDAFVE SqAYARNdg e GDFEKCFAt~ ~~ | |
| <i>A. pediades</i> | S1CtLEAFVE SqKYAreDgq GDFEKCFD~~ ~~ | |
| <i>P. lycii</i> | GvCELsAFVE SqTYARENgq GDFAKCgfvp se | |
| <i>A. terreus</i> 9a1 | GRCKrDAFVA GLSFAQAG.. GNWADCF~~ ~~ | |
| <i>A. terreus</i> cbs | GRCKrDDFVE GLSFARAG.. GNWAECF~~ ~~ | |
| <i>A. niger</i> var. <i>awamori</i> | GRCTrDsFVr GLSFARSG.. GDWAECsA~~ ~~ | |
| <i>A. niger</i> T213 | GRCTrDsFVr GLSFARSG.. GDWAECFA~~ ~~ | |
| <i>A. niger</i> NRRL3135 | GRCTrDsFVr GLSFARSG.. GDWAECFA~~ ~~ | |
| <i>A. fumigatus</i> ATCC13073 | GRCKLNDFVK GLSWARSG.. GNWGECSF~~ ~~ | |
| <i>A. fumigatus</i> ATCC32722 | GRCKLNDFVK GLSWARSG.. GNWGECSF~~ ~~ | |
| <i>A. fumigatus</i> ATCC58128 | GRCKLNDFVK GLSWARSG.. GNWGECSF~~ ~~ | |
| <i>A. fumigatus</i> ATCC26906 | GRCKLNDFVK GLSWARSG.. GNWGECSF~~ ~~ | |
| <i>A. fumigatus</i> ATCC32239 | GRCKLKDFVK GLSWARSG.. GNSEQSFS~~ ~~ | |
| <i>E. nidulans</i> | GRCTLDDWVE GLNFARSG.. GNWktCFTl~ ~~ | |
| <i>T. thermophilus</i> | GRCKrDDDFVr GLSFARqG.. GNWEGCYAas e- | |
| <i>T. lanuginosus</i> | GRCRrDEWIk GLTFARqG.. GHWDrfCF~~ ~~ | |
| <i>M. thermophila</i> | GmCtLERFIE SMAFARGN.. GKWD1CFA~~ ~~ | |
| Consensus Seq. 11 | GRCKLDDFVE GLSFARSG-- GNWAECFA-- -- | |

Fig. 6e

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| | |
|---|-----|
| M G V F V V L L S I A T L F G S T S G T | 20 |
| ATGGGCGTGGTCGTGCTACTGTCCATTGCCACCTGGTTCCACATCCGGTACC | |
| 1 -----+-----+-----+-----+-----+-----+-----+ | 60 |
| TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGAGGCCATGG | |
| A L G P R G N S H S C D T V D G G Y Q C | 40 |
| GCCTTGGGTCTCGTGGTAATTCTCACTCTGTGACACTGTTGACGGTGTTACCAATGT | |
| 61 -----+-----+-----+-----+-----+-----+-----+ | 120 |
| CGGAACCCAGGAGCACCATAAGAGTGAAGAACACTGTGACAACGCCACCAATGGTTACA | |
| F P E I S H L W G T Y S P Y F S L A D E | 60 |
| TTCCCAGAAATTCTCACTTGTGGGTACCTACTCTCCATACTTCTCTTGGCAGACGAA | |
| 121 -----+-----+-----+-----+-----+-----+-----+ | 180 |
| AAGGGTCTTAAAGAGTGAACACCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT | |
| S A I S P D V P D D C R V T F V Q V L S | 80 |
| TCTGCTATTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTCGTTCAAGTTGTCT | |
| 187 -----+-----+-----+-----+-----+-----+-----+ | 240 |
| AGACGATAAAAGAGGTCTGCAAGGTCTGACATCTCAATGAAAGCAAGTTCAAAACAGA | |
| R H G A R Y P T S S A S K A Y S A L I E | 100 |
| AGACACGGTGCTAGATAACCAACTTCTCGCGTCTAAGGTTACTCTGCTTGATTGAA | |
| 241 -----+-----+-----+-----+-----+-----+-----+ | 300 |
| TCTGTGCCACGATCTATGGGTGAAGAACGCGAGATTCCGAATGAGACGAAACTAATT | |
| A I Q K N A T A F K G K Y A F L K T Y N | 120 |
| GCTATTCAAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTGAAGACTTACAAC | |
| 301 -----+-----+-----+-----+-----+-----+-----+ | 360 |
| CGATAAGTTCTGCGATGACGAAAGTCCCATTCATGCGAAAGAACTTCTGAATGTTG | |
| Y T L G A D D L T P F G E N Q M V N S G | 140 |
| TACACTTGGGTGCTGACGACTTGACTCCATTGGTAAAACCAAATGGTTAACTCTGGT | |
| 361 -----+-----+-----+-----+-----+-----+-----+ | 420 |
| ATGTGAAACCCACGACTGCTGAACGTAGGTAAGCCACTTGGTTACCAATTGAGACCA | |
| I K F Y R R Y K A L A R K I V P F I R A | 160 |
| ATTAAGTTCTACAGAACGATACAAGGCTTGGCTAGAAAGATTGTTCCATTAGAGCT | |
| 421 -----+-----+-----+-----+-----+-----+-----+ | 480 |
| TAATTCAAGATGTTCTATGTTCCGAAACCGATTTCTAACAGGTAAGTAATCTCGA | |
| S G S D R V I A S A E K F I E G F Q S A | 180 |
| TCTGGTCTGACAGAGTTATGCTCTGAAAGTTCATGAAAGGTTCCAATCTGCT | |
| 481 -----+-----+-----+-----+-----+-----+-----+ | 540 |
| AGACCAAGACTGTCTCAATAACGAAGACGACTTTCAAGTAACTTCAAAGGTTAGACGA | |
| K L A D P G S Q P H Q A S P V I N V I I | 200 |
| AAGTTGGCTGACCCAGGTTCAACCACCCAAGCTCTCAGTTATAACGTGATCATT | |
| 541 -----+-----+-----+-----+-----+-----+-----+ | 600 |
| TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTCAAGAGGTCAATAATTGCACTAGTAA | |
| P E G S G Y N N T L D H G T C T A F E D | 220 |
| CCAGAAGGATCCGGTTACAACACACTTGGACCACGGTACTTGTACTGCTTCAAGAC | |
| 601 -----+-----+-----+-----+-----+-----+-----+ | 660 |
| GGTCTTCCTAGGCCATGTTGTTGAAACCTGGTGCATGAACATGACGAAAGCTCTG | |

Fig. 7a

23/56

S E L G D D V E A N F T A L F A P A I R
 TCTGAATTAGGTGACGACGTTGAAGCTAACCTCACTGCTTGTGCTCCAGCTATTAGA 240
 661 -----+-----+-----+-----+-----+-----+-----+
 AGACTTAATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTCGATAATCT 720
 A R L E A D L P G V T L T D E D V V Y L
 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTGACTGACGAAGACGTTGTTACTTG 260
 721 -----+-----+-----+-----+-----+-----+-----+
 CGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTCTGCAACAAATGAAC 780
 M D M C P F D T V A R T S D A T E L S P
 ATGGACATGTGTCATTGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCCTCA 280
 781 -----+-----+-----+-----+-----+-----+-----+
 TACCTGTACACAGGTAAGCTGTGACAGCGATCTGAAGACTGCGATGACTTAACAGAGGT 840
 F C A L F T H D E W I Q Y D Y L Q S L G
 TTCTGTGCTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 300
 841 -----+-----+-----+-----+-----+-----+-----+
 AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTCGAACCCCA 900
 K Y Y G Y G A G N P L G P A Q G V G F A
 AAGTACTACGGTTACGGTCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 320
 901 -----+-----+-----+-----+-----+-----+-----+
 TTCATGATGCCAATGCCACGACCATTGGTAACCCAGGTCGAGTCCACAACCAAAGCGA 960
 N E L I A R L T H S P V Q D H T S T N H
 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACAC 340
 961 -----+-----+-----+-----+-----+-----+-----+
 TTGCTTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGAAAGATGATTGGTG 1020
 T L D S N P A T F P L N A T L Y A D F S
 ACTTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGACGCTGACTTCTCT 360
 1021 -----+-----+-----+-----+-----+-----+-----+
 TGAAACCTGAGATTGGTCGATGAAAGGTAACTTGCGATGAAACATGCGACTGAAGAGA 1080
 H D N T M I S I F F A L G L Y N G T K P
 CACGACAACACTATGATATCTATTTCCTCGCTTGGGTTGTACAACGGTACCAAGCCA 380
 1081 -----+-----+-----+-----+-----+-----+-----+
 GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTCGGT 1140
 L S T T S V E S I E E T D G Y S A S W T
 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTGGACT 400
 1141 -----+-----+-----+-----+-----+-----+-----+
 AACAGATGATGAAGACAACCTAGATAACTTCTTGACTGCCAATGAGACGAAGAACCTGA 1200
 V P F A A R A Y V E M M Q C Q A E K E P
 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 420
 1201 -----+-----+-----+-----+-----+-----+-----+
 CAAGGTAAAGCGACGATCTCGAATGCAACTTACTACGTTACAGTTGACTTTCCCTGGT 1260
 L V R V L V N D R V V P L H G C A V D K
 TTGGTTAGAGTTGGTAAAGCAGAGCTTACGTTGCTCATTGCACGGTTGTGCTGTTGACAAG 440
 1261 -----+-----+-----+-----+-----+-----+-----+
 AACCAAATCTAAAACCAATTGCTGCTCAACAAGGTAAACGTGCCAAACACGACAACACTGTT 1320

Fig. 7b

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L G R C K R D D F V E G L S F A R S G G 460
TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGATCTAGACCACCA

N W A E C F A * 467
AACTGGGCTGAATGTTCGCTTAA
1381 -----+-----+----- 1410
TTGACCCGACTTACAAAGCGAATT

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Fig. 7c

M G V F V V L L S I A T L F G S T S G T 20
ATGGGCGTGGTCGTGCTACTGTCCATTGCCACCTGGTTCCACATCCGGTACC
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCACGATGACAGGTAAAGGTGAAACAAGCCAAGGTGAGGCCATGG

A L G P R G N S H S C D T V D G G Y Q C 40
GCCTTGGGTCTCGTGGTAACTCTCACTCTGTGACACTGTTGACGGTGGTTACCAATGT
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTGAGAGTGAGAACACTGTGACAACGTGCCACCAATGGTTACA

F P E I S H L W G T Y S P F F F S L A D E 60
TTCCCAGAAATTCTCACTTGTGGGTACATACTCTCCATTCTCTCTTGGCTGACGAA
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTAAAGAGTGAACACCCCATGTATGAGAGGTAAAGAAGAGAAACCGACTGCTT

S A I S P D V P K G C R V T F V Q V L S 80
TCTGCTATTCTCCAGACGTTCAAAGGGTTAGAGTTACTTCGTTCAAGTTGTCT
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
AGACGATAAAAGAGGTCTGCAAGGTTCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

R H G A R Y P T S S A S K A Y S A L I E 100
AGACACGGTGCTAGATAACCAACTTCTCGGTCTAAGGCGTACTCTGTTGATTGAA
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTGAAGAACGCGAGATTCCGATGAGACGAAACTAACTT

A I Q K N A T A F K G K Y A F L K T Y N 120
GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTGAAGACTTACAAC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
CGATAAGTTCTTGCATGACGAAAGTCCCATTGCGAAAGAAACTCTGAATGTTG

Y T L G A D D L T P F G E Q Q M V N S G 140
TACACTTGGGTGCTGACGACTTGACTCCATTGGTGAACAACAAATGGTTACTCTGGT
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
ATGTGAAACCCACGACTGCTGAACGTGAGGTAAAGCCACTTGTGTTACCAATTGAGACCA

I K F Y R R Y K A L A R K I V P F I R A 160
ATTAAGTTCTACAGAACGATACAAGGCTTGGCTAGAAAGATTGTTCCATTAGAGCT
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTTCTATGTTCCGAAACCGATCTTCAACAAGGTAAAGTAATCTCGA

S G S D R V I A S A E K F I E G F Q S A 180
TCTGGTCTGACAGAGTTATTGCTCTGCTGAAAAGTCATTGAAGGTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGACTTTCAAGTAACCTCAAAGGTAGACGA

K L A D P G A N P H Q A S P V I N V I I 200
AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTCTCCAGTTATTACGTTATTATT
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCACGATTGGGTGTTGAGAGGTCAATAATTGCAATAATAAA

P E G A G Y N N T L D H G L C T A F E E 220
CCAGAACGGTGCTGGTTACAACACACTTGGACCAACGGTTGTGACTGCTTCGAAGAA
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
GGTCTTCCACGACCAATGTTGTTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

Fig. 8a

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S E L G D D V E A N F T A V F A P P I R 240
 TCTGAATTGGGTGACGACGTTGAAGCTAACCTCACTGCTGTTTCGCTCCACCAATTAGA
 661 -----+-----+-----+-----+-----+-----+-----+-----+
 AGACTTAACCCACTGCTGCAACTCGATTGAAGTGACCGACAAAAGCGAGGTGGTTAATCT 720
 A R L E A H L P G V N L T D E D V V N L 260
 GCTAGATTGGAAGCTCACTGCCAGGTGTTAACCTGACTGACGAAGACGTTGTTAACCTG
 721 -----+-----+-----+-----+-----+-----+-----+-----+
 CGATCTAACCTCGAGTGAACGGTCCACAATTGAACTGACTGCTCTGCAACAATTGAAC 780
 M D M C P F D T V A R T S D A T Q L S P 280
 ATGGACATGTGTCATTGCACACTGTTGCTAGAACCTCTGACGCTACTCAATTGTCCTCCA
 781 -----+-----+-----+-----+-----+-----+-----+-----+
 TACCTGTACACAGGTAAGCTGTGACAACGATCTGAAAGACTGCGATGAGTTAACAGAGGT 840
 F C D L F T H D E W I Q Y D Y L Q S L G 300
 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCATCTTTGGGT
 841 -----+-----+-----+-----+-----+-----+-----+-----+
 AAGACACTGAACAAAGTGAGTGCTGTTACCTAACGTTATGCTGATGAAACGTTAGAAACCCA 900
 K Y Y G Y G A G N P L G P A Q G V G F V 320
 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTCGTT
 901 -----+-----+-----+-----+-----+-----+-----+-----+
 TTCATGATGCCAATGCCACGACCATTGGTAACCCAGGTCGAGTTCCACAACCAAAGCAA 960
 N E L I A R L T H S P V Q D H T S T N H 340
 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACAC
 961 -----+-----+-----+-----+-----+-----+-----+-----+
 TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG 1020
 T L D S N P A T F P L N A T L Y A D F S 360
 ACTTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGTACGCTGACTTCTCT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+
 TGAAACCTGAGATTGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA 1080
 H D N T M V S I F F A L G L Y N G T K P 380
 CACGACAAACACTATGGTTCTATTTCTCGCTTGGTTGTACAACGGTACTAACCCA
 1081 -----+-----+-----+-----+-----+-----+-----+-----+
 GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAATGTTGCCATGATTGGT 1140
 L S T T S V E S I E E T D G Y S A S W T 400
 TTGTCTACTACTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTCTGGACT
 1141 -----+-----+-----+-----+-----+-----+-----+-----+
 AACAGATGATGAAGACAACCTAGATAACTTCTTGACTGCCAATGAGACGAAGAACCTGA 1200
 V P F A A R A Y V E M M Q C E A E K E P 420
 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
 1201 -----+-----+-----+-----+-----+-----+-----+-----+
 CAAGGTAAGCGACGATCTCGAATGCAACTTACTACGTTACACTCGACTTTCCCTGGT 1260
 L V R V L V N D R V V P L H G C G V D K 440
 TTGGTTAGAGTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTTGACGAAAG
 1261 -----+-----+-----+-----+-----+-----+-----+-----+
 AACCAATCTCAAAACCAATTGCTGCTCAACAAGGTAACGTTGCAACACCCACAACGTTC 1320

Fig. 8b

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L G R C K R D D F V E G L S F A R S G G 460
TTGGGTAGATGTAAGAGAGACGACTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTCTGCTGAAGCAACTTCAAACAGAAAGCGATCTAGACCACCA

N W E E C F A * 467
AACTGGGAAGAATGTTTCGCTAA
1381 -----+-----+----- 1404
TTGACCCCTTCTAACAAAGCGAATT

0948265 " 0120000

Fig. 8c

M G V F V V L L S I A T L F G S T S G T 20
 ATGGGGGTTTCGCTCGTCTATTATCTATCGCGACTCTGTTCCGCAGCACATCGGGCACT
 1 -----+-----+-----+-----+-----+-----+ 60
 TACCCCCAAAAGCAGCAAGATAATAGATAAGCGCTGAGACAAGCCGTGCTAGCCCGTGA

 A L G P R G N H S K S C D T V D L G Y Q 40
 GCGCTGGGCCCGTGAAATCACTCCAAGTCCTCGGATACGGTAGACCTAGGGTACCAAG
 61 -----+-----+-----+-----+-----+-----+ 120
 CGCGACCCGGGGCACCTTAGTGAGGTTCAAGGACGCTATGCCATCTGGATCCCATGGTC

 C S P A T S H L W G T Y S P Y F S L E D 60
 TGCTCCCCTGCGACTTCTCATCTATGGGGCACGTACTGCCATaCTTTCGCTCGAGGAC
 121 -----+-----+-----+-----+-----+-----+ 180
 ACGAGGGGACGCTGAAGAGTAGATAACCCGtgCATGAGCGGTatGAAAAGCGAGCTCCTG

 E L S V S S K L P K D C R I T L V Q V L 80
 GAGCTGTCCGTGTCGAGTAAGCTCCAAAGGATTGCCGATCACCTGGTACAGGTGCTA
 181 -----+-----+-----+-----+-----+-----+ 240
 CTCGACAGGCACAGCTATTGAAGGGTCTAACGGCTAGTGGAACCATGTCCACGAT

 S R H G A R Y P T S S K S K K Y K K L I 100
 TCGCGCCATGGAGCGCGTACCCAACCAGCTCCAAGAGCAAAAGTATAAGAAGCTTaTt
 241 -----+-----+-----+-----+-----+-----+ 300
 AGCGCGGTACCTCGGCCATGGGTTGGTCGAGGTTCTCGTTTCAATTCTCGAAAtAa

 T A I Q A N A T D F K G K Y A F L K T Y 120
 ACGGCGATCCAGGCAATGCCACCGACTCAAGGGCAAGTAcGCCTTTGAAGACGTAC
 301 -----+-----+-----+-----+-----+-----+ 360
 TGCCGCTAGGTCCGGTACGGTGGCTGAAGTTCCGTTCAAtgCGGAAAACCTCTGCATG

 N Y T L G A D D L T P F G E Q Q L V N S 140
 AACTATACTCTGGGTGCGGATGACCTCACTCCCTTGGGGAGCAGCAGCTGGTGAACCTCG
 361 -----+-----+-----+-----+-----+-----+ 420
 TTGATATGAGACCCACGCCTACTGGAGTGAGGGAAACCCCTCGTCGTCGACCAACTGAGC

 G I K F Y Q R Y K A L A R S V V P F I R 160
 GGCATCAAGTTCTACCAAGGAGGTACAAGGCTCTGGCGCGCAGTGTGGTGCCTTATTGCG
 421 -----+-----+-----+-----+-----+-----+ 480
 CCGTAGTTCAAGATGGTCTCCATGTTCCGAGACCGCGCGTCACACCACGGCAAATAAGCG

 A S G S D R V I A S G E K F I E G F Q Q 180
 GCCTCAGGCTCGGACGGGTTATTGCTTCGGAGAGAAGTTCATCGAGGGGTTCCACAGCAG
 481 -----+-----+-----+-----+-----+-----+ 540
 CGGAGTCCGAGCCTGGCCAATAACGAAGCCCTCTTCAAGTAGCTCCCCAAGGTGTC

 A K L A D P G A T N R A A P A I S V I I 200
 GCGAAGCTGGCTGATCCTGGCGCGACGAACCGCGCGCTCCGGCGATTAGTGTGATTATT
 541 -----+-----+-----+-----+-----+-----+ 600
 CGCTTCGACCGACTAGGACCGCGCTGCTGGCGCGAGGCCGCTAATCACACTAATAA

 P E S E T F N N T L D H G V C T K F E A 220
 CGGAGAGCGAGACGTTCAACAATACGCTGGACCAAGGTGTGACGAAGTTGAGGCG
 601 -----+-----+-----+-----+-----+-----+ 660
 GGCCTCTCGCTCTGCAAGTTGTTATGCGACCTGGTGCACACACGTGCTCAAACACTCCGC

Fig. 9a

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S Q L G D E V A A N F T A L F A P D I R 240
 AGTCAGCTGGGAGATGAGGTTGCCAATTCACTGCGCTTTGCACCCGACATCCGA
 661 -----+-----+-----+-----+-----+-----+ 720
 TCAGTCGACCCCTACTCCAACGCCGGTAAAGTGACGCGAGAACGTGGCTGTAGGCT

A R L E K H L P G V T L T D E D V V S L 260
 GCTCGCtCGAGAACATCTCCTGGCGTGACGCTGACAGACGAGGACGTGTCAGTCTA
 721 -----+-----+-----+-----+-----+-----+ 780
 CGAGCGgAGCTCTCGTAGAAGGACCGCACTGCGACTGTCTGCTCCTGCAACAGTCAGAT

M D M C P F D T V A R T S D A S Q L S P 280
 ATGGACATGTGTCGTTGATAACGGTAGCGCGACCAGCGACGCAAGTCAGCTGTCACCG
 781 -----+-----+-----+-----+-----+-----+ 840
 TACCTGTACACAgGCAAACATGCCATCGCGCGTGGTCGCTGGTCAAGTCGACAGTGGC

F C Q L F T H N E W K K Y D Y L Q S L G 300
 TTCTGTCAACTCTTCACTCACAAATGAGTGGAAAGTACgACTACCTTCAGTCCTTGGGC
 841 -----+-----+-----+-----+-----+-----+ 900
 AAGACAGTTGAGAAGTGAGTGTAACTCACCTTCTTCATGcTGATGGAAGTCAGGAACCCG

K Y Y G Y G A G N P L G P A Q G I G F T 320
 AAGTACTACGGCTACGGCGCAGGCAACCCCTCTGGGACCGGCTCAGGGGATAGGGTTCA
 901 -----+-----+-----+-----+-----+-----+ 960
 TTCATGATGCCGATGCCCGTCCGGTGGAGACCCCTGGCGAGTCCCCTATCCCAAGTGG

N E L I A R L T R S P V Q D H T S T N S 340
 AACGAGCTGATTGCCCGGTTGACgCGTCGCCAGTGCAGGACCACACCAGCACTAACTCG
 961 -----+-----+-----+-----+-----+-----+ 1020
 TTGCTCGACTAACGGGCAACTGcGCAAGCGGTACGTCTGGTGTGGTGTGATTGAGC

T L V S N P A T F P L N A T M Y V D F S 360
 ACTCTAGTCTCAACCCGCCACCTCCCGTTGAAACGCTACCATGTACGTCGACTTTCA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 TGAGATCAGAGGTTGGCCGGTGGAAAGGGCAACTTGCATGGTACATGCAAGCTGAAAAGT

H D N S M V S I F F A L G L Y N G T E P 380
 CACGACAACAGCATGGTTCCATCTTGCATTGGCCTGTACAACGGCACTGAACCC
 1081 -----+-----+-----+-----+-----+-----+ 1140
 GTGCTGTTGTCGTACCAAGGTAGAAGAACGTAACCCGGACATGTTGCCGTGACTTGGG

L S R T S V E S A K E L D G Y S A S W V 400
 TTGTCCCGGACCTCGGTGGAAAGGCCAAGGAATTGGATGGTATTCTGCATCCTGGTG
 1141 -----+-----+-----+-----+-----+-----+ 1200
 AACAGGGCCTGGAGCCACCTTCGCGTTCTAACCTACCCATAAGACGTAGGACCCAC

V P F G A R A Y F E T M Q C K S E K E P 420
 GTGCCTTCGGCGCGAGCCTACTTCGAGACGATGCAATGCAAGTCGAAAAGGAGCCT
 1201 -----+-----+-----+-----+-----+-----+ 1260
 CACGGAAAGCCGCGCGCTCGGATGAAGCTCTGCTACGTTACGTTAGCCTTCCCTCGGA

L V R A L I N D R V V P L H G C D V D K 440
 CTTGTTCGCGCTTGATTAATGACCGGGTTGTGCCACTGCATGGCTGCGATGTGGACAAG
 1261 -----+-----+-----+-----+-----+-----+ 1320
 GAACAAAGCGCGAAACTAATTACTGGCCCAACACGGTGACGTACCGACGCTACACCTGTC

Fig. 9b

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L G R C K L N D F V K G L S W A R S G G 460
CTGGGGCGATGCAAGCTGAATGACTTGTCAAGGGATTGAGTTGGGCCAGATCTGGGGC
1321 -----+-----+-----+-----+-----+-----+ 1380
GACCCCGCTACGTTGACTTACTGAAACAGTTCCCTAACTCAACCCGGTAGACCCCCG

N W G E C F S * 467
AACTGGGGAGAGTGCTTTAGTTGA
1381 -----+-----+----- 1404
TTGACCCCTCTCACGAAATCAACT

CP-1
 ECO RI M G V F V V L L S I A T L F G S T
TATATGAATTCATGGCGTGTCTCGTGCTACTGTCATTGCCACCTGTTCGGTTCCA
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 ATATACTTAAGTACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAGCCAAGGT

S G T A L G P R G N S H S C D T V D G G
CATCCGGTACCGCCTGGTCCTCGTGTTAATTCTCACTCTGTGACACTGTTGACGGTG
 61 -----+-----+-----+-----+-----+-----+-----+ 120
GTAGGCCATGGCGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCAC

CP-2
 CP-3
 Y Q C F P E I S H L W G Q Y S P Y F S L
GTTACCAATGTTCCCAGAAATTCTCACTGTGGGTCAATACTCTCCATACTTCTCTT
 121 -----+-----+-----+-----+-----+-----+-----+ 180
CAATGGTTACAAAGGGTCTTAAAGAGTGAAACACCCAGTTATGAGAGGTATGAAGAGAA

E D E S A I S P D V P D D C R V T F V Q
TGGAAGACGAATCTGCTATTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTCGTT
 181 -----+-----+-----+-----+-----+-----+-----+ 240
ACCTTCTGCTTAGACGATAAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAG

CP-4.7
CP-5.7
 V L S R H G A R Y P T D S K G K K Y S A
AAGTTTGTCTAGACACGGTGTAGATACCCAACTgacTCTAAGggtaAGaagTACTCTG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
TTCAAAACAGATCTGTGCCACGATCTATGGGTTGactgAGATTCCcaTTCttcATGAGAC

L I E A I Q K N A T A F K G K Y A F L K
CTTGATTGAAGCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTTGA
 301 -----+-----+-----+-----+-----+-----+-----+ 360
GAAACTAACCGATAAGTTCTTGCAGACGAAAGTCCCATTCAATGCGAAAGAACT

CP-6
 CP-7
 T Y N Y T L G A D D L T P F G E N Q M V
AGACTTACAACACTACACTGGGTGCTGACGACTTGACTCCATTGGTGA~~AAAACCAAATGG~~
 361 -----+-----+-----+-----+-----+-----+-----+ 420
TCTGAATGTTGATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTGGTTACC

N S G I K F Y R R Y K A L A R K I V P F
TTAACTCTGGTATTAAGTTCTACAGAACGATACAAGGCTTGGCTAGAAAGATTGTTCCAT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTCAACAAAGGTA

CP-8.7
CP-9
 I R A S G S S R V I A S A E K F I E G F
TCATTAGAGCTCTGGTCTtctAGAGTTATTGCTCTGCTGAAAGTTCAATTGAAGGTT
 481 -----+-----+-----+-----+-----+-----+-----+ 540
AGTAATCTCGAAGACCAAGAagaTCTCAATAACGAAGACGACTTTCAAGTAACCTCCAA

Q S A K L A D P G S Q P H Q A S P V I D
TCCAATCTGCTAAGTTGGCTGACCCAGGGTCTCAACCACACCAAGCTTCTCCAGTTATTG
 541 -----+-----+-----+-----+-----+-----+-----+ 600
AGGTTAGACGATTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTCGAAGAGGTCAATAAC

Fig. 10a

CP-10.7

CP-11.7

V I I S E A S S Y N N T L D P G T C T A
 ACGTTATTATTtctGacgctTCTtctTACAACAACTTTGGACccaaGGTACTTGTACTG
 601 -----+-----+-----+-----+-----+-----+ 660
 TGCAATAATAAagaCTgcgaAGGagaATGTTGTTGTGAAACCTGggctCCATGAACATGAC

F E D S E L A D T V E A N F T A L F A P
 CTTTCGAAGACTCTGAATTGgctGAcactGTTGAAGCTAACCTCACTGCTTGCGCTC
 661 -----+-----+-----+-----+-----+-----+ 720
 GAAAGCTTCTGAGACTAACcgaaCTGtgaCAAACCTCGATTGAAGTGACGAAACAAGCGAG

CP-12.7

A I R A R L E A D L P G V T L T D T E V
 CAGCTATTAGAGCTAGATTGGAAGCTGACTGCCAGGTGTTACTTGACTGACactgaaG
 721 -----+-----+-----+-----+-----+-----+ 780
 GTCGATAATCTCGATCTAACCTCGACTGAACGGTCCACAATGAAAATGACTGtgaacttC

CP-13.7

T Y L M D M C S F E T V A R T S D A T E
 TTactTACTTGATGGACATGTGTTctTTCGAAACTGTTGCTAGAACTTCTGACGCTACTG
 781 -----+-----+-----+-----+-----+-----+ 840
 AAatgaATGAACTACCTGTACACAagaAAGCTTGACAACGATTTGAAGACTGCGATGAC

L S P F C A L F T H D E W R H Y D Y L Q
 AATTGTCCTCATTCTGTGCTTGTTCACTCACGACGAATGGAGAcactTACGACTACTTGC
 841 -----+-----+-----+-----+-----+-----+ 900
 TTAACAGAGGTAAAGACACGAAACAAGTGAGTGCTGCTTACCTCTgtgATGCTGATGAC

CP-14.7

CP-15.7

S L K K Y Y G H G A G N P L G P T Q G V
 AATCTTGAAGAAGTACTACGGTcacGGTGTGGTAACCCATTGGGTCCAactCAAGGTG
 901 -----+-----+-----+-----+-----+-----+ 960
 TTAGAAACttcTTCATGATGCCAgtgCCACGACCATTGGTAACCCAGGTtgaGTTCCAC

G F A N E L I A R L T R S P V Q D H T S
 TTGGTTTCGCTAACGAATTGATTGCTAGATTGACTAGATCTCAGTTCAAGACCACACTT
 961 -----+-----+-----+-----+-----+-----+ 1020
 AACCAAAGCGATTGCTTAACTAACGATCTAACTGATCTAGAGGTCAAGTTCTGGTGTGAA

CP-16

CP-17.7

T N H T L D S N P A T F P L N A T L Y A
 CTACTAACACACTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGTACG
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GATGATTGGTGTAAACCTGAGATTGGTCATGAAAGGGTAACCTTGCATGAAACATGC

D F S H D N G I I S I F F A L G L Y N G
 CTGACTTCTCTCACGACAAACggattATTCTATTCTCGCTTGGTTGTACAACG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 GACTGAAGAGAGTGCTGTTGccataaTAAAGATAAAAGAAGCGAAACCCAAACATGTTGC

CP-18.7

CP-19.7

T A P L S T T S V E S I E E T D G Y S S
 GTACTGCTCCATTGTCTACTACTTCTGTGAATCTATTGAAGAAACTGACGGTTACTCTt
 1141 -----+-----+-----+-----+-----+-----+ 1200
 CATGACGAGGTAAACAGATGATGAAGACAACCTAGATAACTTCTTGTACTGCCAATGAGAa

Fig. 10b

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A W T V P F A S R A Y V E M M Q C Q A E
 ctgctTGGACTGTTCCATTcgttctAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
 1201 -----+-----+-----+-----+-----+-----+ 1260
 gacgaACCTGACAAGGTAAGcgaagaTCTCGAATGCAACTTACTACGTTACAGTTCGAC
 CP-20
 CP-21
 K E P L V R V L V N D R V V P L H G C A
 AAAAGGAACCATTGGTTAGAGTTTGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
 1261 -----+-----+-----+-----+-----+-----+ 1320
 TTTTCCTTGGTAACCAATCTCAAAACCAATTGCTGTCACAACAGGTAACGTGCCAACAC
 V D K L G R C K R D D F V E G L S F A R
 CTGTTGACAAGTTGGTAGATGTAAGAGAGACGACTCGTTGAAGGTTGTCTTCGCTA
 1321 -----+-----+-----+-----+-----+-----+ 1380
 GACAACTGTTCAACCCATCTACATTCTCTGCTGAAGCAACTCCAAACAGAAAGCGAT
 CP-22
 S G G N W A E C F A * Eco RI
 GATCTGGTGGTAACTGGGCTGAATGTTCGCTTAAGAATTATATA
 1381 -----+-----+-----+-----+-----+ 1426
 CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT

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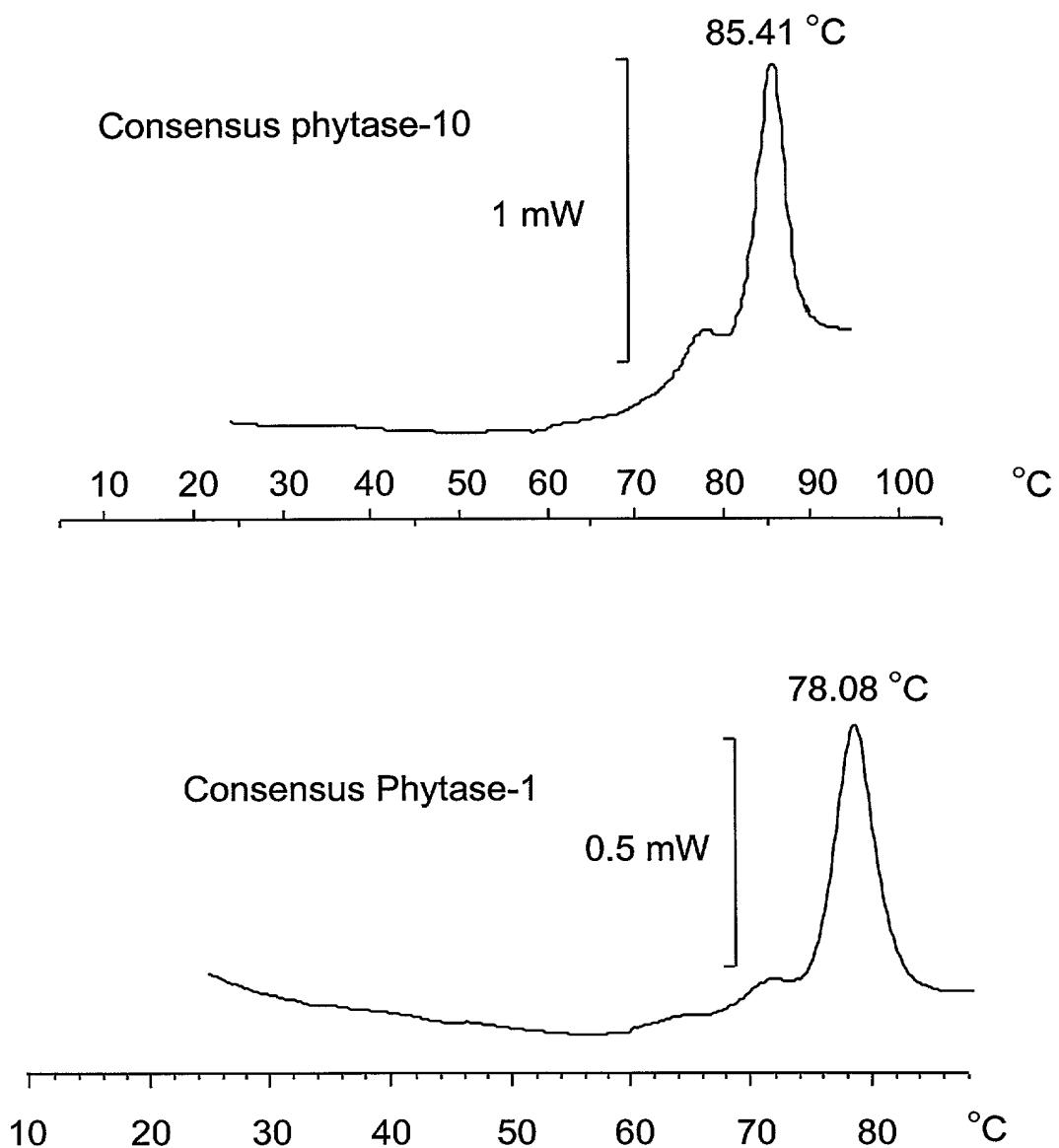


Fig. 11

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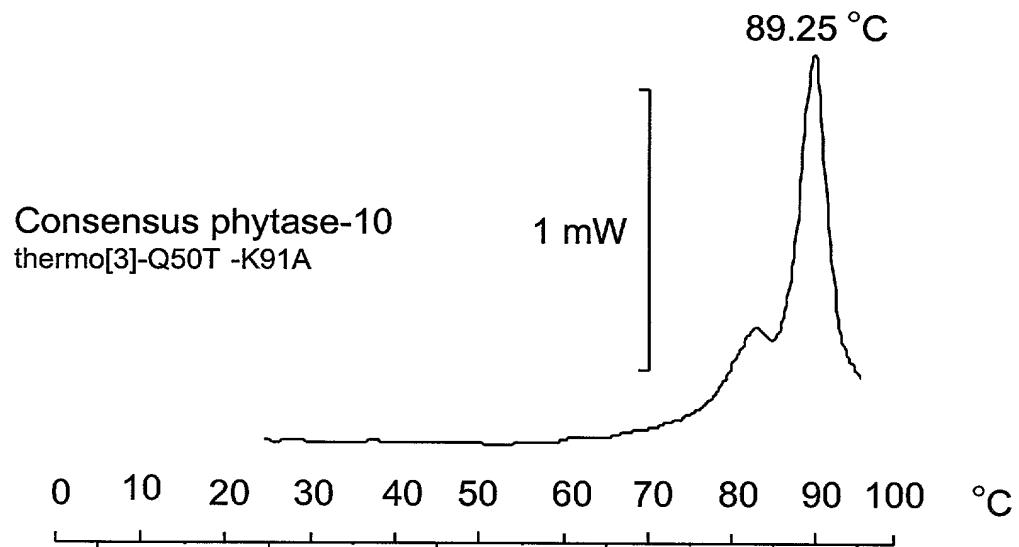
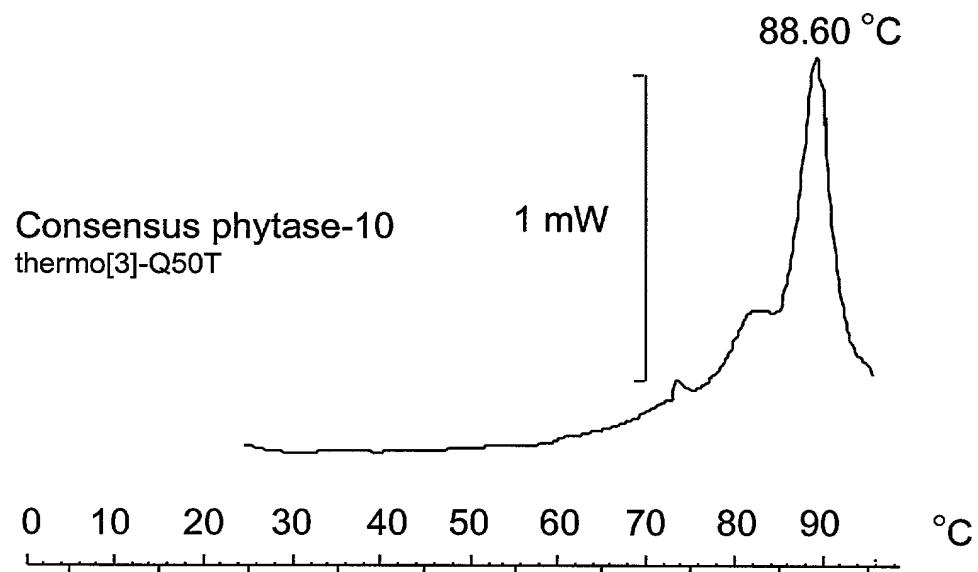


Fig. 12

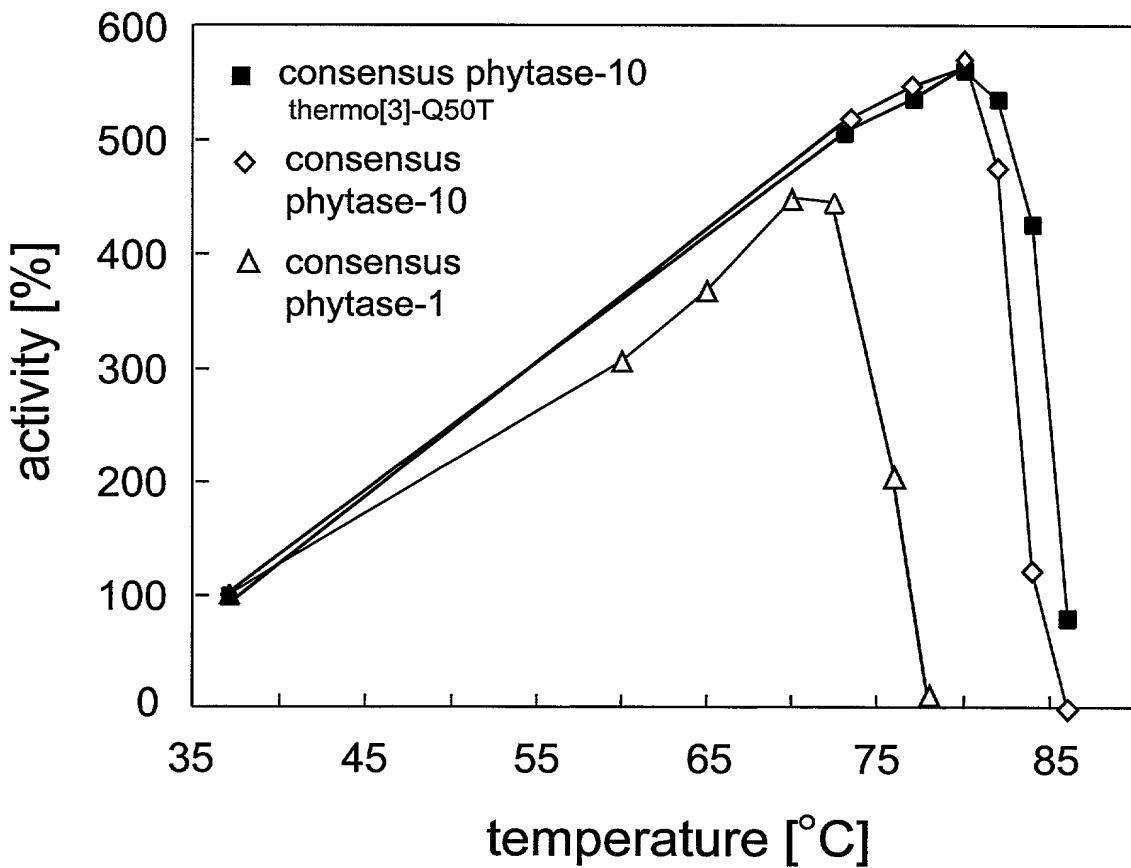


Fig. 13

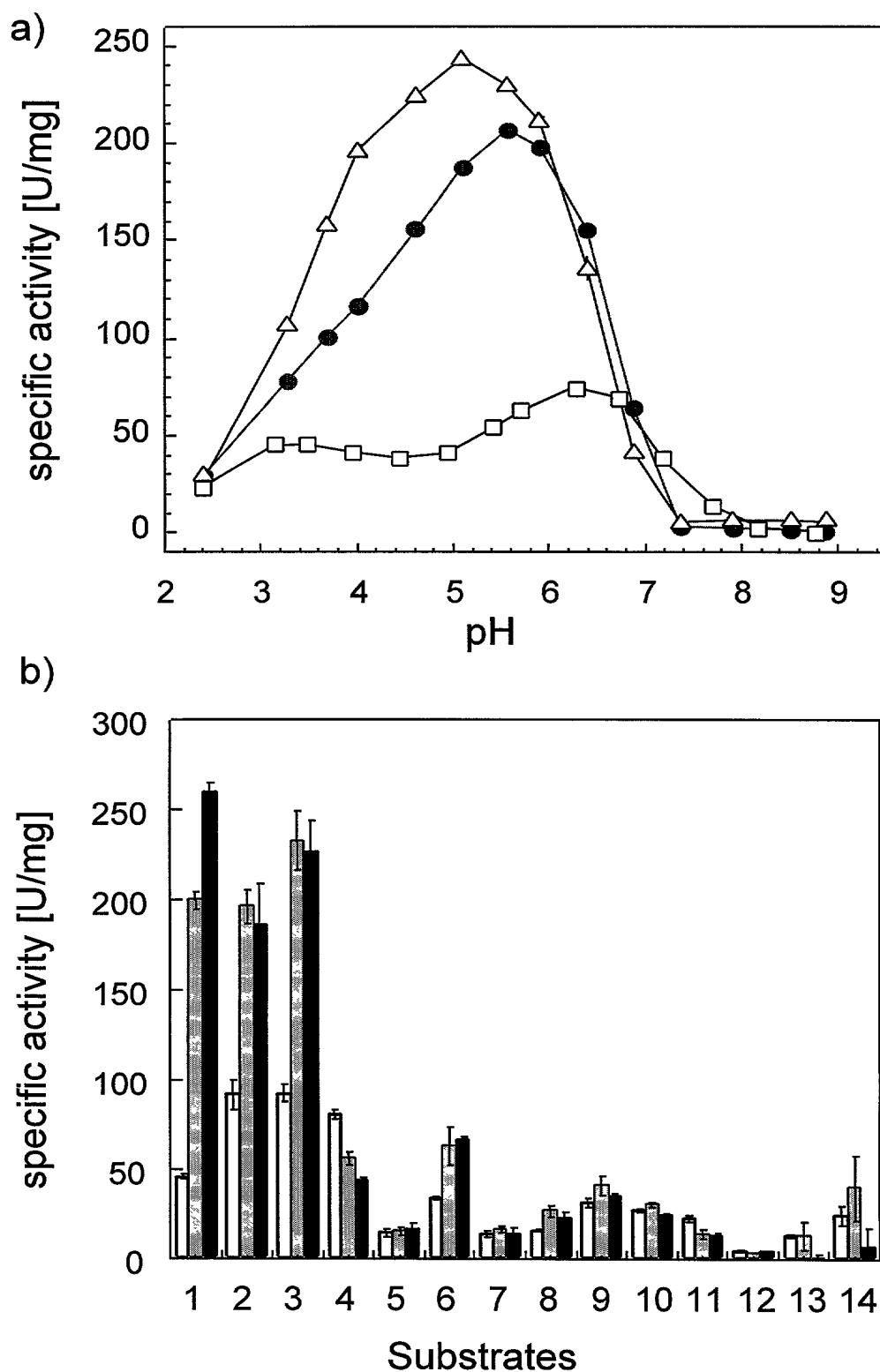


Fig. 14

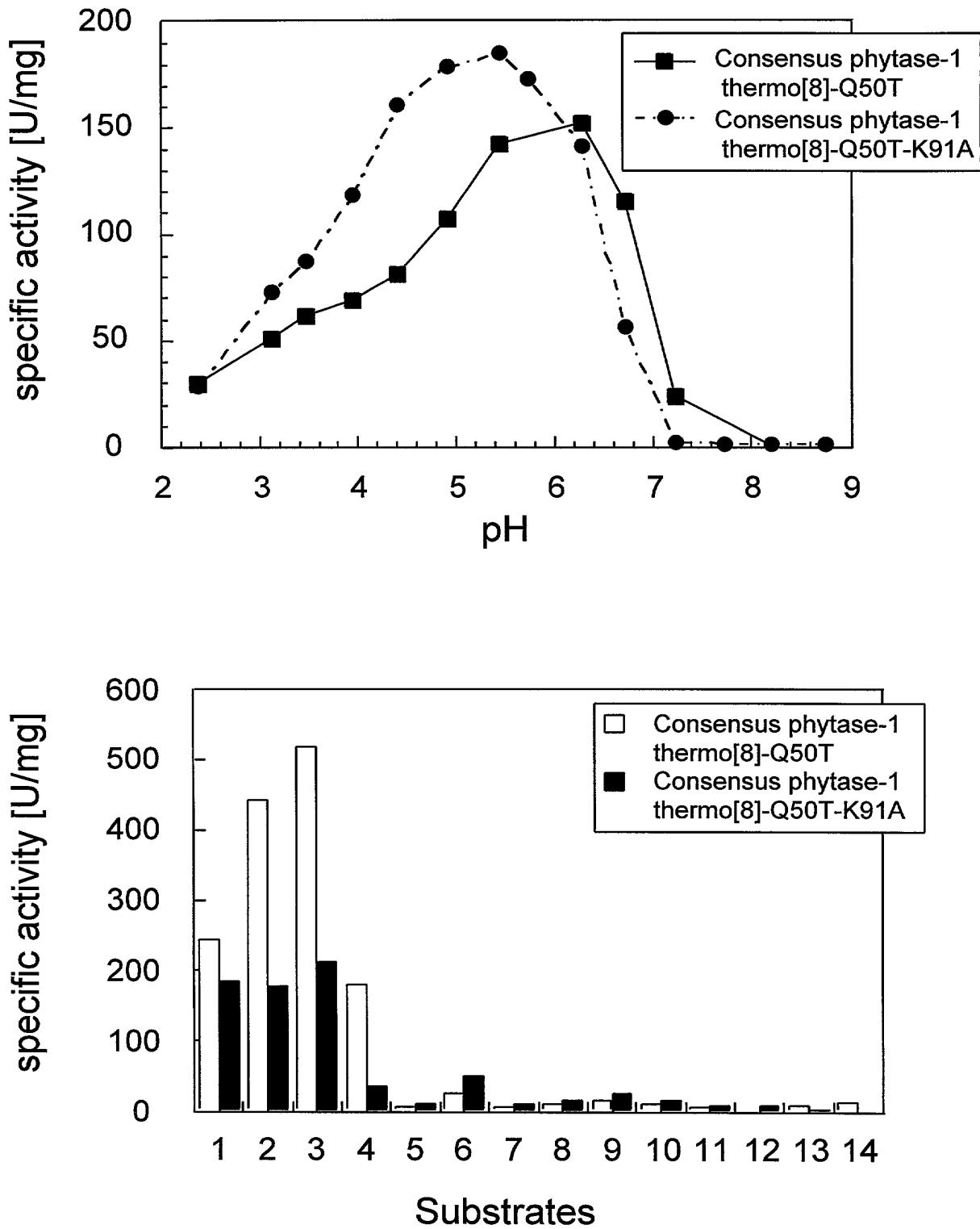


Fig. 15

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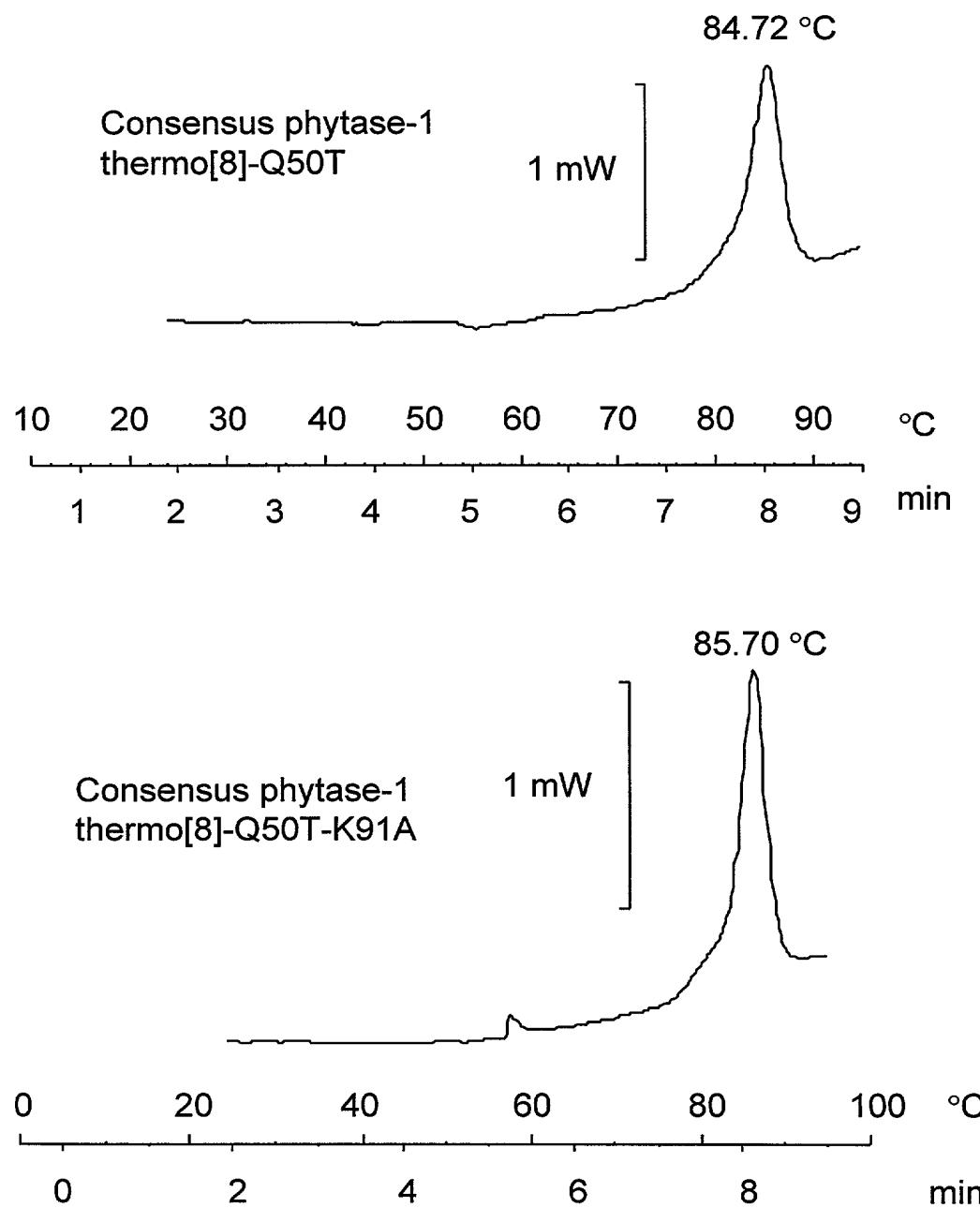


Fig. 16

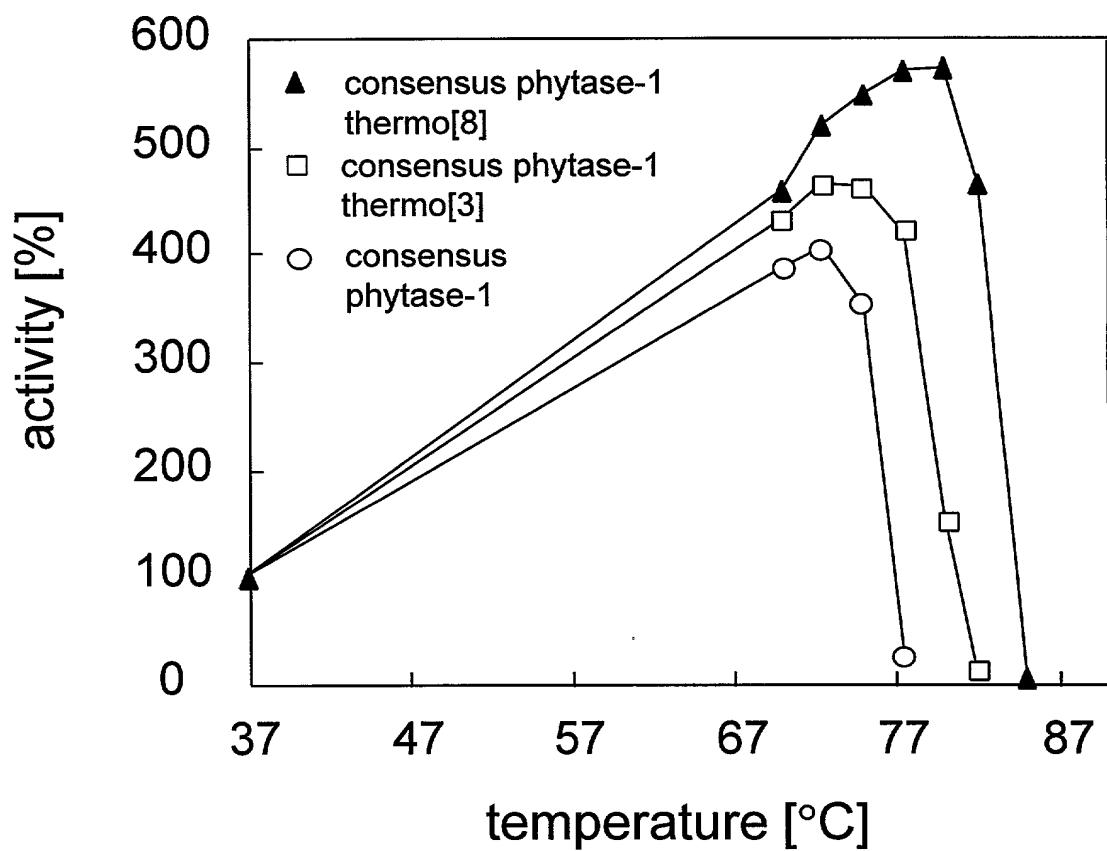


Fig. 17

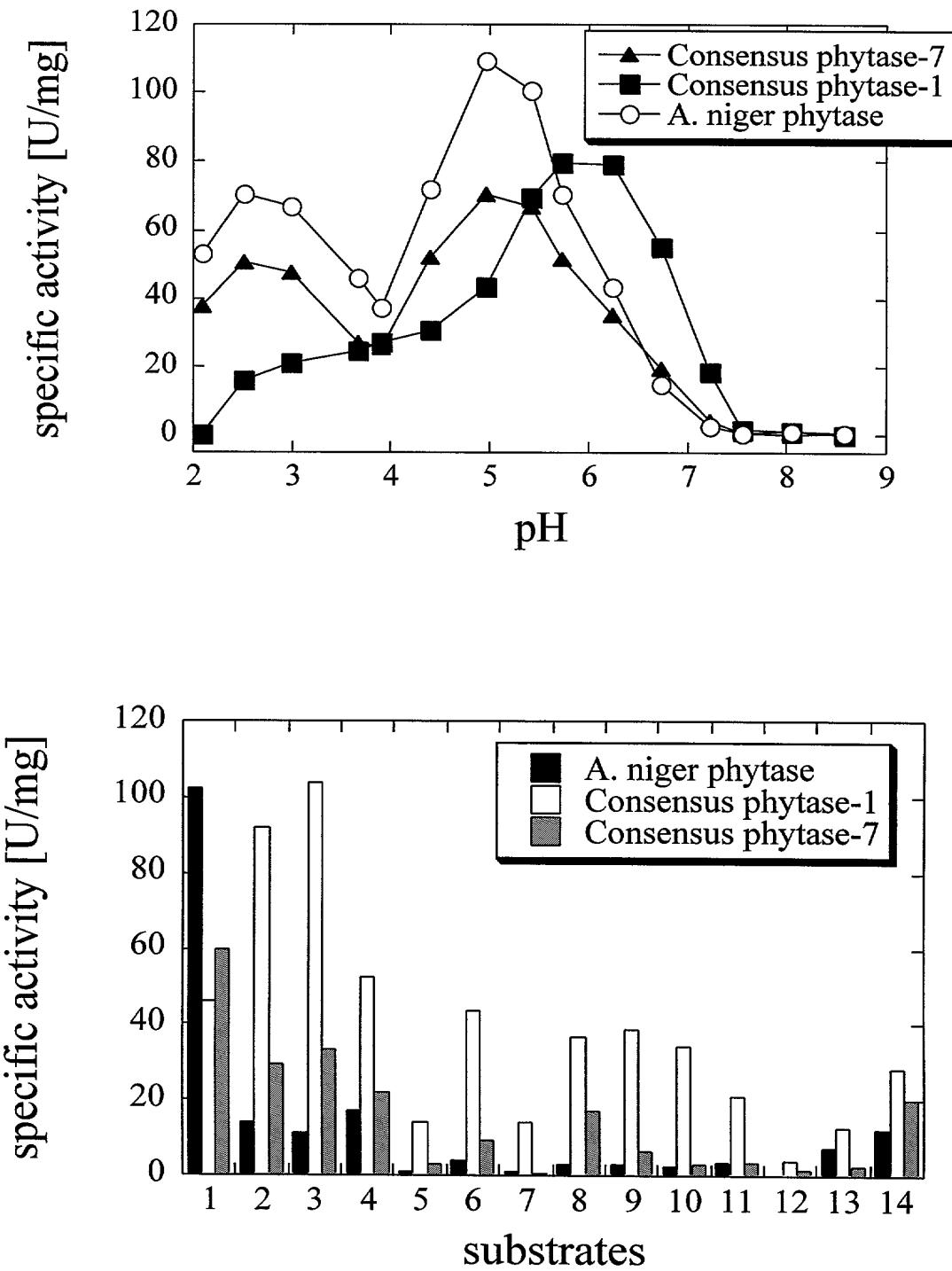


Fig. 18

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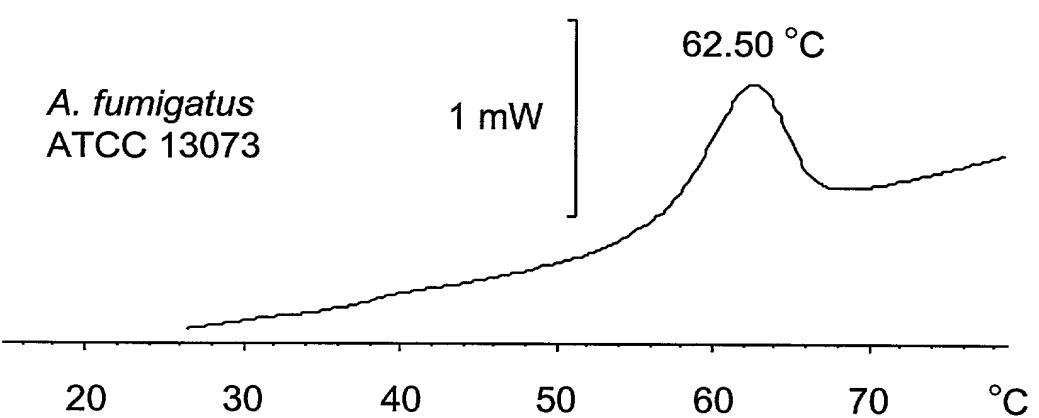
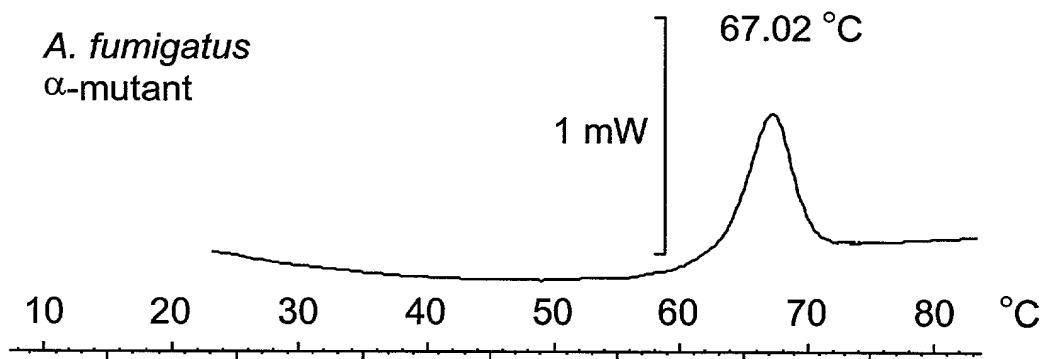


Fig. 19

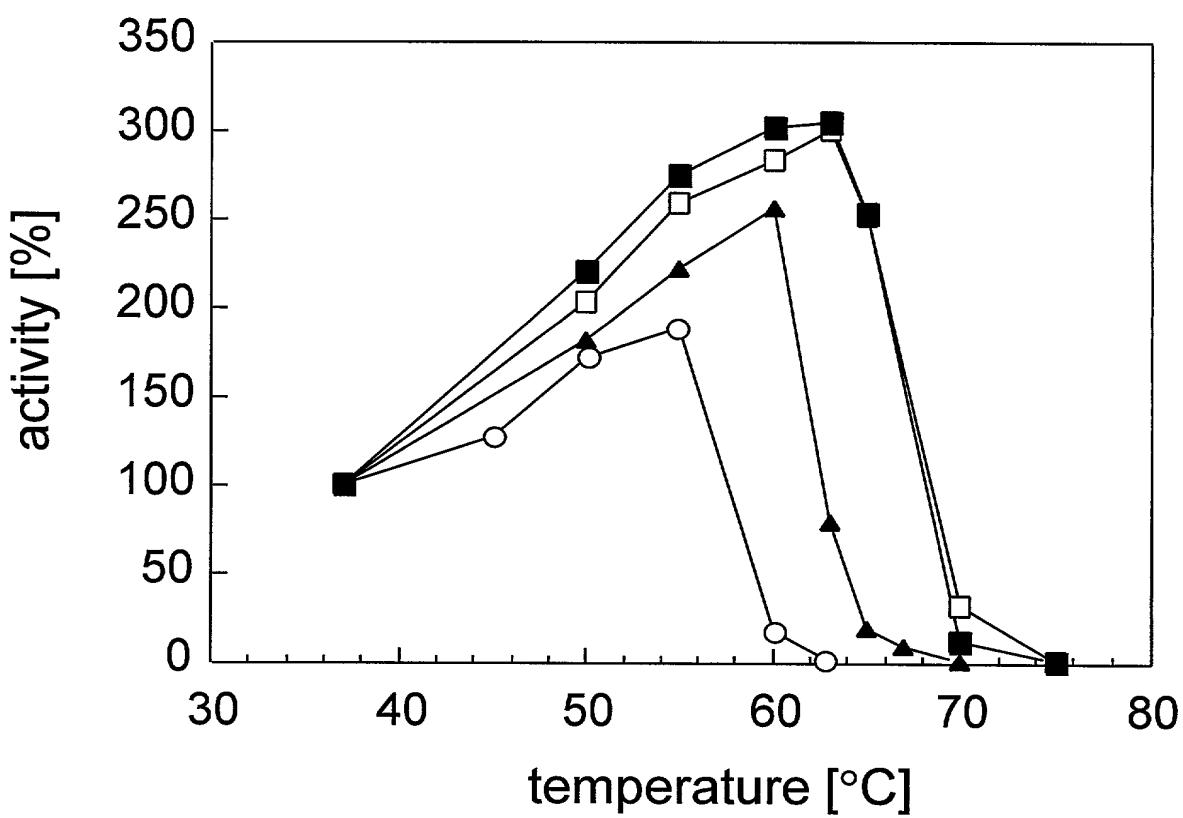


Fig. 20

1 MGVFVVLLSI ATLFGSTSGT ALGPRGNSHS CDTVDGGYQC FPEISSNWSP

51 YSPYFSLADE SAISPDVPKG CRVTFVQVLQ RHGARFPTSG AATRISALIE

101 AIQKNATAFK GKYAFLKTYN YTLGADDLVP FGANQSSQAG IKFYRRYKAL

151 ARKIVPFIRA SGSDRVIDSA TNWIEGFQSA KLADPGANPH QASPVINII

201 PEGAGYNNTL DHGLCTAFAEE SELGDDVEAN FTAVFAPP*IR* ARLEAHLPV

251 NLTDEDVVNL MDMCPFD**TVA** RTSDATELSP FCDLFTHDEW IQYDYLGDLD

301 KYYGTGAGNP LGPAQGVGFV NELIARLTHS PVQDHSTNH TLDSNPATFP

351 LNATLYADFS HDNTMVAIFF ALGLYNGTKP LSTTSVESIE ETDGYSASWL

401 VPFSARMYVE MMQCEAEKEP LVRVLVNDRV VPLHGCGVDK LGRCKRDDFV

451 EGLSFARSGG NWEECFA

DRAFT2005-020000

ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGGTTCCACATCCGGTACC
 1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
 TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGTAGGCCATGG

 M G V F V V L L S I A T L F G S T S G T -

 GCCTTGGGTCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
 61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
 CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGTGCCACCAATGGTTACA

 A L G P R G N S H S C D T V D G G Y Q C -

 TTCCCAGAAATTCTCACTTGTGGGTACCTACTCTCCATACTTCTCTTGGCAGACGAA
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 AAGGGTCTTAAAGAGTGAAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

 F P E I S H L W G T Y S P Y F S L A D E -

 TCTGCTATTCCTCCAGACGTCCAAAGGACTGTAGAGTTACTTCGTTCAAGTTTGCT
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 AGACGATAAAGAGGTCTGCAGGGTTCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

 S A I S P D V P K D C R V T F V Q V L S -

 AGACACGGTGCTAGATAACCAACTTCTTAAGTCTAAGGCTTACTCTGCTTGATTGAA
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
 TCTGTGCCACGATCTATGGGTTGAAGAAGATTCACTCCGAATGAGACGAAACTAACCT

 R H G A R Y P T S S K S K A Y S A L I E -

 GCTATTCAAAGAACGCTACTGCTTCAAGGTAAGTACGCTTCTGAAGACTTACAAC
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
 CGATAAGTTTCTTGCATGACGAAAGTCCCATTCAATGCGAAAGAACTTCTGAATGTTG

 A I Q K N A T A F K G K Y A F L K T Y N -

 TACACTTTGGGTGCTGACGACTTGAUTCCATTGGTAAAACCAAATGGTTAATCTGGT
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
 ATGTGAAACCCACGACTGCTGAUTGAGGTAAGCCACTTTGGTTACCAATTGAGACCA

 Y T L G A D D L T P F G E N Q M V N S G -

 ATTAAGTTCTACAGAAGATAACAGGCTTGGCTAGAAAGATTGTTCCATTCAATTAGAGCT
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
 TAATTCAAGATGTCTTCTATGTTCCGAACCGATCTTCTAACAGGTAAGTAATCTCGA

 I K F Y R R Y K A L A R K I V P F I R A -

 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCAATTGAAGGTTCCAATCTGCT
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 AGACCAAGACTGTCTCAATAACGAAGACGACTTTCAAGTAACCTCCAAAGGTTAGACGA

 S G S D R V I A S A E K F I E G F Q S A -

Fig. 22a

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AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAAACGTGATCATT
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTCAAGAGGTCAATAATTGCACTAGTAA

 K L A D P G S Q P H Q A S P V I N V I I -

 CCAGAAGGGATCCGGTTACAACAAACACTTGGACCATGGCTTTGTACTGCCTTCGAAGAC
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 GGTCTTCCTAGGCCAATGTTGTGAAACCTGGTACCAAGAACATGACGAAAGCTTCTG

 P E G S G Y N N T L D H G L C T A F E D -

 TCTACCCTAGGTGACGACGTTGAAGCTAACCTCACTGCTTGCTCCAGCTATTAGA
 661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
 AGATGGGATCCACTGCTGCAACTCGATTGAAGTGACGAAACAAAGCGAGGTCGATAATCT

 S T L G D D V E A N F T A L F A P A I R -

 GCTAGATTGGAAGCTGACTTGCAGGTGTTACTTGACTGACGAAGACGTTACTTG
 721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
 CGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTCTGCAACAAATGAAC

 A R L E A D L P G V T L T D E D V V Y L -

 ATGGACATGTGTCCATTGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
 781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
 TACCTGTACACAGGTAAGCTGTGACAGCGATCTGAAGACTGCGATGACTAACAGAGGT

 M D M C P F D T V A R T S D A T E L S P -

 TTCTGTGCTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
 841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
 AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTATGCTGATGAACGTTTCGAACCCA

 F C A L F T H D E W I Q Y D Y L Q S L G -

 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGTCCAGCTCAAGGTGTTGGTTCGCT
 901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
 TTCATGATGCCAATGCCACGACCATTGGTAACCCAGGTGAGTTCCACAACCAAAGCGA

 K Y Y G Y G A G N P L G P A Q G V G F A -

 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTCAAGACCAACTTCTACTAACAC
 961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
 TTGCTTAACGATCTAACGACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

 N E L I A R L T H S P V Q D H T S T N H -

 ACTTTGGACTCTAACCCAGCTACTTTCCATTGAACGCTACTTGACTGCTGACTTCTCT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 TGAAACCTGAGATTGGTCGATGAAAGGGTAACGGCATGAAACATGCGACTGAAGAGA

 T L D S N P A T F P L N A T L Y A D F S -

Fig. 22b

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D94982552020000

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CACGACAAACACTATGATATCTATTCTCGTTGGGTTGTACAACGTACCAAGCCA
1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACTATAGATAAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

H D N T M I S I F F A L G L Y N G T K P -
TTGTCTACTACTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTCTGGACT
1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTAGATAACTCTTGACTGCCAATGAGACGAAGAACCTGA

L S T T S V E S I E E T D G Y S A S W T -
GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAGCTGAAAGGAACCA
1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTGCAATGCAACTTACTACGTTACAGTTGACTTTCCCTGGT

V P F A A R A Y V E M M Q C Q A E K E P -
TTGGTTAGAGTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
AACCAATCTCAAAACCAATTGCTGTCTAACAAAGGTAACGTGCCAACACGACAACGTTC

L V R V L V N D R V V P L H G C A V D K -
TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTGCTGAAGCAAACAGAAAGCGATCTAGACCACCA

L G R C K R D D F V E G L S F A R S G G -
AACTGGGCTGAATGTTCGCTTAA
1381 -----+-----+-----+-----+-----+-----+-----+-----+ 1404
TTGACCCGACTTACAAAGCGAATT

N W A E C F A *

```

Fig. 22c

ATGGGCGTGGTCGTGCTACTGTCCATTGCCACCTGGTCCACATCCGGTACC
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGAGGCCATGG

 M G V F V V L L S I A T L F G S T S G T -

 GCCTTGGGTCTCGTGGTAATTCTCACTCTGTGACACTGTTGACGGTGGTTACCAATGT
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGTGCCACCAATGGTTACA

 A L G P R G N S H S C D T V D G G Y Q C -

 TTCCCAGAAATTCTCACTTGTGGGTACCTACTCTCCATACTTCTCTGGCAGACGAA
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 AAGGGTCTTAAAGAGTGAAACACCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

 F P E I S H L W G T Y S P Y F S L A D E -

 TCTGCTATTCCTCCAGACGTCCAAAGGACTGTAGAGTTACTTCGTTCAAGTTGTCT
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 AGACGATAAAGAGGTCTGCAGGGTTCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

 S A I S P D V P K D C R V T F V Q V L S -

 AGACACGGTGCTAGATAACCAACTTCTCGGTCTAAGGCTTACTCTGCTTGATTGAA
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TCTGTGCCACGATCTATGGGTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAACCT

 R H G A R Y P T S S A S K A Y S A L I E -

 GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTGAAGACTTACAAC
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 CGATAAGTTTCTTGCATGACGAAAGTCCCATTGCGAAAGAACTTCTGAATGTTG

 A I Q K N A T A F K G K Y A F L K T Y N -

 TACACTTTGGGTGCTGACGACTTGACTCCATTGGTAAAACCAAATGGTTAATCTGGT
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 ATGTGAAACCCACGACTGCTGAAGTGGCACTTTGGTTACCAATTGAGACCA

 Y T L G A D D L T P F G E N Q M V N S G -

 ATTAAGTTCTACAGAAGATAACAAGGCTTGGCTAGAAAGATTGTTCCATTAGAGCT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TAATTCAAGATGTCTTCTATGTTCCGAACCGATCTTCTAACAGGTAAGTAATCTCGA

 I K F Y R R Y K A L A R K I V P F I R A -

 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTCCAATCTGCT
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 AGACCAAGACTGTCTCAATAACGAAGACGACTTTCAAGTAACCTCCAAAGGTTAGACGA

 S G S D R V I A S A E K F I E G F Q S A -

Fig. 23a

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AAGTTGGCTGACCCAGGTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
 541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
 TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTCGAAGAGGTCAATAATTGCACTAGTAA

 K L A D P G S Q P H Q A S P V I N V I I -

 CCAGAAGGGATCCGGTTACAACAAACACTTGGACCATGGCTTTGTACTGCCTTCGAAGAC
 601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
 GGTCTTCCTAGGCCAATGTTGTTGAAACCTGGTACCAAGAACATGACGAAAGCTTCTG

 P E G S G Y N N T L D H G L C T A F E D -

 TCTACCCCTAGGTGACGACGTTGAAGCTAACCTCACTGCTTGCTCCAGCTATTAGA
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
 AGATGGGATCCACTGCTGCAACTCGATTGAAGTGACGAAACAAAGCGAGGTCGATAATCT

 S T L G D D V E A N F T A L F A P A I R -

 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTGACTGACGAAGACGTTGTTACTTG
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
 CGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTTCTGCAACAAATGAAC

 A R L E A D L P G V T L T D E D V V Y L -

 ATGGACATGTGTCCATTGACACTGTCGCTAGAACCTCTGACGCTACTGAATTGTCTCCA
 781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
 TACCTGTACACAGGTAAGCTGTGACAGCGATCTGAAGACTGCGATGACTAACAGAGGT

 M D M C P F D T V A R T S D A T E L S P -

 TTCTGTGCTTGTTCACTCACGACGAATGGATCCAATCGACTACTTGCAAAGCTTGGGT
 841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 AAGACACGAAACAAGTGAGTGCTGTTACCTAGGTATGCTGATGAACGTTTCGAACCCA

 F C A L F T H D E W I Q Y D Y L Q S L G -

 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGTCCAGCTCAAGGTGTTGGTTCGCT
 901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
 TTCACTGATGCCAATGCCACGACCATTGGTAACCCAGGTGAGTTCCACAACCAAAGCGA

 K Y Y G Y G A G N P L G P A Q G V G F A -

 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCAACTTCTACTAACAC
 961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
 TTGCTTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

 N E L I A R L T H S P V Q D H T S T N H -

 ACTTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGACTGCTGACTTCTCT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
 TGAAACCTGAGATTGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

 T L D S N P A T F P L N A T L Y A D F S -

Fig. 23b

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CACGACAACACTATGATATCTATTTCTCGCTTGGGTTGTACAACGGTACCAAGCCA
 1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
 GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTCGTT

 H D N T M I S I F F A L G L Y N G T K P -

 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAAATGACGGTTACTCTGCTCTGGACT
 1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
 AACAGATGATGAGACAACCTTAGATAACTCTTGACTGCCAATGAGACGAAGAACCTGA

 L S T T S V E S I E E T D G Y S A S W T -

 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
 1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
 CAAGGTAAGCGACGATCTGAATGCAACTTACTACGTTACAGTTCGACTTTCCCTGGT

 V P F A A R A Y V E M M Q C Q A E K E P -

 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
 1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
 AACCAAATCTCAAAACCAATTGCTGCTCAACAAGGTAACGTGCCAACACGACAACGTTC

 L V R V L V N D R V V P L H G C A V D K -

 TTGGGTAGATGTAAGAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
 1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
 AACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGATCTAGACCACCA

 L G R C K R D D F V E G L S F A R S G G -

 AACTGGGCTGAATGTTCGCTTAA
 1381 -----+-----+-----+-----+-----+-----+-----+-----+ 1404
 TTGACCCGACTTACAAAGCGAATT

 N W A E C F A *

Fig. 23c

ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGGTCCACATCCGGTACC
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAGCCAAGGTGTAGGCCATGG

 M G V F V V L L S I A T L F G S T S G T -

 GCCTTGGGTCTCGTGGTAATTCTCACTCTGTGACACTGTTGACGGTGGTACCAATGT
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGTGCCACCAATGGTTACA

 A L G P R G N S H S C D T V D G G Y Q C -

 TTCCCAGAAATTCCTCACTTGTGGGTACATACTCTCCATTCTCTTTGGCTGACGAA
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 AAGGGTCTTAAAGAGTGAAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

 F P E I S H L W G T Y S P F F S L A D E -

 TCTGCTATTCCTCCAGACGTTCAAAGGGTTGTAGAGTTACTTCGTTCAAGTTTGCT
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 AGACGATAAAAGAGGTCTGCAAGGTTCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

 S A I S P D V P K G C R V T F V Q V L S -

 AGACACGGTGCTAGATAACCAACTTCTCTAAAGTCTAAGGCTTACTCTGCTTGATTGAA
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TCTGTGCCACGATCTATGGGTTGAAGAAGATTCAAGATTCCGAATGAGACGAAACTAACCTT

 R H G A R Y P T S S K S K A Y S A L I E -

 GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTGAAGACTTACAAT
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 CGATAAGTTTCTTGCATGACGAAAGTTCCCATTGCGAAAGAAACTCTGAATGTTA

 A I Q K N A T A F K G K Y A F L K T Y N -

 TACACTTTGGGTGCTGACGACTTGACTCCATTGGTGAACAACAAATGGTTAATCTGGT
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 ATGTGAAACCCACGACTGCTGAAGTGGCACTTGTGTTACCAATTGAGACCA

 Y T L G A D D L T P F G E Q Q M V N S G -

 ATTAAGTTCTACAGAAGATAACAGGCTTGGCTAGAAAGATTGTTCCATTAGAGCT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TAATTCAAGATGTCTTCTATGTTCCGAACCGATCTTCTAACAGGTAAGTAATCTCGA

 I K F Y R R Y K A L A R K I V P F I R A -

 TCTGGTTCTGACAGAGTTATTGCTTCTGCCGAAAAGTTCAATTGAAGGTTCCAATCTGCT
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 AGACCAAGACTGTCTCAATAACGAAGACGGCTTCAAGTAACCTCCAAAGGTTAGACGA

 S G S D R V I A S A E K F I E G F Q S A -

Fig. 24a

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DRAFT

AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTCTCCAGTTATTAACGTTATTATT
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 TTCAACCGACTGGGTCCACGATTGGGTGTTCGAAGAGGTCAATAATTGCAATAATAA

 K L A D P G A N P H Q A S P V I N V I I -

 CCAGAAGGTGCTGGTTACAACAACACTTGGACCACGGTTGTACTGCTTCGAAGAA
 601 -----+-----+-----+-----+-----+-----+ 660
 GGTCTTCCACGACCAATGTTGTTGAAACCTGGTGCCAACACATGACGAAAGCTTCTT

 P E G A G Y N N T L D H G L C T A F E E -

 TCTACCCTAGGTGACGACGTTGAAGCTAACCTCACTGCTGTTTCGCTCCACCAATTAGA
 661 -----+-----+-----+-----+-----+-----+ 720
 AGATGGGATCCACTGCTGCAACTTCGATGAAAGTGACGACAAAAGCGAGGTGGTTAATCT

 S T L G D D V E A N F T A V F A P P I R -

 GCTAGATTGGAAGCTCACTGCCAGGTGTTAACCTGACTGACGAAGACGTTGTTAACCTG
 721 -----+-----+-----+-----+-----+-----+ 780
 CGATCTAACCTTCGAGTGAAACGGTCCACAATTGAACTGACTGCTTCTGCAACAAATTGAAC

 A R L E A H L P G V N L T D E D V V N L -

 ATGGACATGTGTCATTGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGCTCCA
 781 -----+-----+-----+-----+-----+-----+ 840
 TACCTGTACACAGGTAAGCTGTGACAACGATCTGAAGACTGCGATGAGTTAACAGAGGT

 M D M C P F D T V A R T S D A T Q L S P -

 TTCTGTACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTGGGT
 841 -----+-----+-----+-----+-----+-----+ 900
 AAGACACTGAACAAGTGAGTGCTGCTTACCTAACGTTATGCTGATGAACGTTAGAAACCCA

 F C D L F T H D E W I Q Y D Y L Q S L G -

 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGTCCAGCTCAAGGTGTTGGTTCGTT
 901 -----+-----+-----+-----+-----+-----+ 960
 TTCATGATGCCAATGCCACGACCATTGGTAACCCAGGTGAGTTCCACAACCAAAGCAA

 K Y Y G Y G A G N P L G P A Q G V G F V -

 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCAACTTCTACTAACCCAC
 961 -----+-----+-----+-----+-----+-----+ 1020
 TTGCTTAACGATCTAACGACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

 N E L I A R L T H S P V Q D H T S T N H -

 ACTTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGACTGCTGACTTCTCT
 1021 -----+-----+-----+-----+-----+-----+ 1080
 TGAAACCTGAGATTGGTCGATGAAAGGGTAACCTGCGATGAAACATGCGACTGAAGAGA

 T L D S N P A T F P L N A T L Y A D F S -

Fig. 24b

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CACGACAACACTATGGTTCTATTTCTCGCTTGGTTGTACAACGGTACTAAGCCA
 1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
 GTGCTGTTGTGATACCAAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTGGT

 H D N T M V S I F F A L G L Y N G T K P -

 TTGTCTACTACTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTGGACT
 1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
 AACAGATGATGAAGACAACCTAGATAACTCTTTGACTGCCAATGAGACGAAGAACCTGA

 L S T T S V E S I E E T D G Y S A S W T -

 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
 1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
 CAAGGTAAGCGACGATCTGAATGCAACTTACTACGTTACACTTCGACTTTCCCTGGT

 V P F A A R A Y V E M M Q C E A E K E P -

 TTGGTTAGAGTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
 1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
 AACCAATCTCAAAACCAATTGCTGTCTAACAAAGGTAACGTGCCAACACGACAACGTTC

 L V R V L V N D R V V P L H G C A V D K -

 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
 1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
 AACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGATCTAGACCACCA

 L G R C K R D D F V E G L S F A R S G G -

 AACTGGGAAGAATGTTTCGCTTAA
 1381 -----+-----+-----+-----+-----+-----+-----+-----+ 1404
 TTGACCCCTTCTTACAAAGCGAATT

 N W E E C F A *

Fig. 24c

DRAFT_2005

ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGGTCCACATCCGGTACC
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAGCCAAGGTGTAGGCCATGG

 M G V F V V L L S I A T L F G S T S G T -

 GCCTTGGGTCTCGTGGTAATTCTCACTCTGTGACACTGTTGACGGTGGTTACCAATGT
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACGTGCCACCAATGGTTACA

 A L G P R G N S H S C D T V D G G Y Q C -

 TTCCCAGAAATTCCTCACTTGTGGGTACATACTCTCCATTCTCTTTGGCTGACGAA
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 AAGGGTCTTAAAGAGTGAAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

 F P E I S H L W G T Y S P F F S L A D E -

 TCTGCTATTCTCCAGACGTTCAAAGGGTTGTAGAGTTACTTCGTTCAAGTTTGCT
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 AGACGATAAAGAGGCTGCAAGGTTCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

 S A I S P D V P K G C R V T F V Q V L S -

 AGACACGGTGCTAGATAACCAACTTCTCTCGGTCTAAGGCTTACTCTGCTTGATTGAA
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAACTT

 R H G A R Y P T S S A S K A Y S A L I E -

 GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAGTACGCTTCTGAAGACTTACAAT
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 CGATAAGTTTCTTGCATGACGAAAGTCCCATTGCGAAAGAAACTTCTGAATGTTA

 A I Q K N A T A F K G K Y A F L K T Y N -

 TACACTTTGGGTGCTGACGACTTGACTCCATTGGTGAACAAACAAATGGTTAATCTGGT
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 ATGTGAAACCCACGACTGCTGAAGTGGCACTTGTGTTACCAATTGAGACCA

 Y T L G A D D L T P F G E Q Q M V N S G -

 ATTAAGTTCTACAGAAGATAACAGGCTTGGCTAGAAAGATTGTTCCATTAGAGCT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTCTAACAGGTAAGTAATCTCGA

 I K F Y R R Y K A L A R K I V P F I R A -

 TCTGGTTCTGACAGAGTTATTGCTTCTGCCGAAAAGTTCAATTGAAGGTTCCAATCTGCT
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 AGACCAAGACTGTCTCAATAACGAAGACGGCTTTCAAGTAACCTCCAAGGTTAGACGA

 S G S D R V I A S A E K F I E G F Q S A -

Fig. 25a

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DQ526626 DQ422000

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AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTCTCCAGTTATTAACGTTATTATT
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
      TTCAACCGACTGGGTCCACGATTGGGTGTTCGAAGAGGTCAATAATTGCAATAATAA

      K L A D P G A N P H Q A S P V I N V I I -
      CCAGAAGGTGCTGGTTACAACAACACTTGGACCACGGTTGTACTGCTTCGAAGAA
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
      GGTCTTCCACGACCAATGTTGTTGAAACCTGGTGCCAACACATGACGAAAGCTTCTT

      P E G A G Y N N T L D H G L C T A F E E -
      TCTACCCTAGGTGACGACGTTGAAGCTAACCTCACTGCTGTTTCGCTCCACCAATTAGA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
      AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAACCT

      S T L G D D V E A N F T A V F A P P I R -
      GCTAGATTGGAAGCTCACCGCCAGGTGTTAACCTGACTGACGAAGACGTTGTTAACCTG
721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
      CGATCTAACCTTCGAGTGAAACGGTCCACAATTGAACtgactgcttctgcaacaattgaac

      A R L E A H L P G V N L T D E D V V N L -
      ATGGACATGTGTCCATTGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
      TACCTGTACACAGGTAAAGCTGTGACAACGATCTGAAGACTGCGATGAGTTAACAGAGGT

      M D M C P F D T V A R T S D A T Q L S P -
      TTCTGTGACTTGTTCACTCAGGACGAATGGATTCAATACGACTACTTGCAATCTTGGGT
841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
      AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

      F C D L F T H D E W I Q Y D Y L Q S L G -
      AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTCGTT
901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
      TTCATGATGCCAATGCCACGACCATTGGTAACCCAGGTGAGTTCCACAACCAAAGCAA

      K Y Y G Y G A G N P L G P A Q G V G F V -
      AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCAACTTCTACTAACCCAC
961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
      TTGCTTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

      N E L I A R L T H S P V Q D H T S T N H -
      ACTTTGGACTCTAACCCAGCTACTTCCCATTGAACGCTACTTGACTGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
      TGAAACCTGAGATTGGTCGATGAAAGGGTAACCTGCGATGAAACATGCGACTGAAGAGA

      T L D S N P A T F P L N A T L Y A D F S -

```

Fig. 25b

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CACGACAACACTATGGTTCTATTCTCGTTGGGTTGTACAACGGTACTAAGCCA
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140
 GTGCTGTTGTGATACCAAAAGATAAAAGAAGCGAACCAAACATGTTGCCATGATTGGT

 H D N T M V S I F F A L G L Y N G T K P -

 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAAAGTACGGTTACTCTGCTCTTGGACT
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200
 AACAGATGATGAAGACAACCTAGATAACTCTTGACTGCCAATGAGACGAAGAACCTGA

 L S T T S V E S I E E T D G Y S A S W T -

 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 CAAGGTAAGCGACGATCTGAATGCAACTTACTACGTTACACTTCGACTTTCCCTGGT

 V P F A A R A Y V E M M Q C E A E K E P -

 TTGGTTAGAGTTGGTTAACGACAGAGTTGTCATTGCACGGTTGTGCTGTTGACAAG
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320
 ACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACGTTC

 L V R V L V N D R V V P L H G C A V D K -

 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380
 ACCCATCTACATTCTCTGCTGAAGCAACTTCAAACAGAAAGCGATCTAGACCACCA

 L G R C K R D D F V E G L S F A R S G G -

 AACTGGGAAGAATGTTCGTTAA
 1381 -----+-----+-----+-----+ 1404
 TTGACCCCTTCTTACAAAGCGAATT

 N W E E C F A *

Fig. 25c

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
 (Includes Reference to PCT International Applications)

Attorney's Docket Number:
5808.200-US

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Improved Phytases

The specification of which (check only one item below):

- [] is attached hereto
 was filed as United States application

Application No. To Be Assigned

on January 20, 2000

and was amended

on _____

[] was filed as PCT international application
 Number _____

on _____

and was amended under PCT Article 19

on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by an amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim priority benefits under Title 35, United States Code, §119 of any provisional or foreign application(s) for patent or inventor's certificate or of any PCT international applications(s) for patent or inventor's certificate or of any PCT international applications(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

PRIOR U.S. PROVISIONAL/FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 U.S.C. 119:

| COUNTRY (if PCT, indicated "PCT") | APPLICATION NUMBER | DATE OF FILING (day, month, year) | PRIORITY CLAIMED UNDER 35 USC 119 |
|--------------------------------------|--------------------|--------------------------------------|--------------------------------------|
| Denmark | PA 1999 00092 | 22 January 1999 | [X] YES [] NO |
| Denmark | PA 1999 01340 | 21 September 1999 | [X] YES [] NO |
| United States | 60/117,659 | 28 January 1999 | [X] YES [] NO |
| United States | 60/156,495 | 28 September 1999 | [X] YES [] NO |
| | | | [] YES [] NO |

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
 (Includes Reference to PCT International Applications)

Attorney's Docket Number:
5808.200-US

I hereby claim the benefit under Title 35, United States Code '120 of any United States application(s) or PCT international application(s) designating the United States of America that is/are listed below and, insofar as the subject matter of each of the claims of this applications is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of Title 35, United States Code, '112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, '1 56(a) which occurred between the filing date of the prior application(s) and the national or PCT international filing date of this application.

**PRIOR U S. APPLICATIONS OR PCT INTERNATIONAL APPLICATIONS DESIGNATING THE U.S. FOR BENEFIT
UNDER 35 U S C. 120**

| U S APPLICATIONS | | | STATUS (Check one) | | |
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| U S APPLICATION NUMBER | U S FILING DATE | | Patented | Pending | Abandoned |
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| PCT APPLICATIONS DESIGNATING THE U.S. | | | | | |
| APPLICATION NO | FILING DATE | US SERIAL NUMBERS ASSIGNED (if any) | | | |
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| POWER OF ATTORNEY. As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith Steve T Zelson Elias J Lambiris Valeta A Gregg Carol E Rozek Robert L Starnes Reza Green, Reg No 30,335 Reg No 33,728 Reg No 35,127 Reg No 36,993 Reg No 41,324 Reg No 38,475 | | | | | |
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COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY
 (Includes Reference to PCT International Applications)

Attorney's Docket Number:
S808.200-US

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon

| | | |
|-------------------------|-------------------------|-------------------------|
| Signature of Inventor 1 | Signature of Inventor 2 | Signature of Inventor 3 |
| Date | Date | Date |
| Signature of Inventor 4 | Signature of Inventor 5 | Signature of Inventor 6 |
| Date | Date | Date |
| Signature of Inventor 7 | Signature of Inventor 8 | Signature of Inventor 9 |
| Date | Date | Date |